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U7930 Orgyia pseu
S64501 p8.9=8,9 kd
AX766573 Sequence
AY043265 Epiphyas
AY145471 Rachiplus
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AF512031 Choriston
D14467 Bombyx mori
M59422 Autographa
U59461 Mamestra co
AF246708 Spodopter
AF325155 Spodopter
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L22858 Autographa
AY327402 Choriston
BD187790 A virus i
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12.8 153656 12.1 15528 12.1 15528 12.1 1307592 11.6 13611 11.6 13611 11.3 131403 11.3 1314	BD070856 BD070856 BD070856 BD070856.1 GI:22616459 JP 2001516225-A/1. unidentified M unidentified unclassified. 1 (bases 1 to 564) Grigllatti, T.A., Theilmann, D.A., Pfeife Insect expression vectors Patent: JP 2001516225-A 1 25-SEP-2001; THE UNIVERSITY OF BRITISH COLUMBIA OS Multicapsid nucleopolyhedrovirus PN 2001516225-A/1	PP 25.SEP-2001 PR 26.AMR-1998 JP 19 PR 27.MAR-1999 US THOWAS A GRIGILATTI.DA A PERIFER, DWAYNE D. PI HEGEDUS CC INSECT EXPRESSION FH Key CC INSECT EXPRESSION FT SOURCE FT SOURCE Organism "un / mol_type="ge"/
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/ Codon start=1
/ product="Unknown"
/ produ
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                                                                                                                                                                                                                                                                                                                                           complement(6129. .6791)
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/codon_start=1
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9893. .11362
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pseudotsugata multicapsid
Genomic, 1429 nt].
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1 (bases 1 to 1429)

Wu,X., Stewart,S. and Theilmann,D.A.

Mu,X., stewart,S. and Theilmann,D.A.

protein from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

Olyhedrosis virus

Olynol. 74 (Pt 8), 1591-1598 (1993)
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                                                                                                                         128172 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                    128232 TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGCCAGTCACGTAGGCCCGGCCTTATC
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                                                                                              1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                       TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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                                            Indels
; DB 14;
1.3e-170;
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                                               0; Mismatches
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p8.9=8.9 kda basic protein [Orgyia
nuclear polyhedrosis virus OpMNPV,
  Score 564;
Pred. No. 1
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100.0%;
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S64501.1 GI:404518
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Acadaism="synthetic construct"
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561. .561.
/note="HindIII site"
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100.0%; Pred. No. 8.6e-166;
tive 0; Mismatches 0;
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                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Aval, Smal,
2551. .2556
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'note="ApaLI site"
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/note="Aval site"
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/note="Clai site"
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284. .2289
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2294. .2299
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/note="BamHI
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204. .2209
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| db_xref="a[1:404519"
| trainslation="MNSWOKIRMAKQQVRVARQHRAAKLGRLYKAKKLRAELCEKLQ
LQRVNNDAALAKAFEEEFVYPHFSFYLYTLN"
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larity 99.8%; Pred. No. 1.6e-170;
Conservative 0; Mismatches 1; Indels 0;
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           /gene="p8.9"
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763. .990
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Sequence 60 from Patent WO03042244.
AX766573
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.2090)
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VGMNNEYRISLAKKGGGCPIMNIHSEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPLTPHQVPPPPPPPPTTPLQGLLPVRDVEATPSPPSTLSKSTTLDEPETFSNASMIQ
PPVPPTREIL PVRPHILKEKTII ISBLPDMPATNNIDDQGLAPAPPPPPPPPPPPP
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IKKGVTLKPSKTNKSDKKVDDRADLINSI KIGVKLKPIKVNTNQPLPBAPVTDISVIA
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Epiphyas postvittana nucleopolyhedrovirus, complete genome.
AY043265
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LANIVSRVEHLLRYEIVNDVEITTLSGDFYEEYSKYAARQYALSIQMPPPPPVITPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTLKKRRANISQSESSSESNSSQSWDEBGNTQTIRKANKDHLKYAVNLYNFFATTHAY
RTNSELPKLLDNVFSLLDRKPRSVENVNEAKNILDNIKERVKLTSNQLDNAEAQSLYI
NDPNQFYIQVEDLIFAGRYADAKMHLDLAITESGNDERLRRLKKFANDLDAVVV"
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and Ward,V.K.
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Submitted (03-JUL-2001) Microbiology, University of Otago,
                                                                                                                                                                                                                                                                                                                                                Epiphyas postvittana nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequence of the Epiphyas postvittana
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                                                                        CATCTGTT 552
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114732 CTACGAATCGTAGACTATTTAACTTGAATAGTCTACACTGTTCTATACGCTCCTAATACA 114673
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Rachiplusia ou multiple nucleopolyhedrovirus, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rachiplusia ou multiple nucleopolyhedrovirus'
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Bonning, B.C. and Harrison, R.L.
Direct Submission
Submitted (28-AUG-2002) Entomology, Iowa State University, Ames,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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join[(131515. 131526,1. .326)
hore="consists of 30 bp imperfect palindromes; hrl;
replication origin"
                                                                                                                                                                                                                                                                                                                 Rachiplusia ou multiple nucleopolyhedrovirus
Rachiplusia ou multiple nucleopolyhedrovirus
Viruses; dabNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
1 (bases 248 to 8029)
Harrison, R.L. and Bonning, B.C.
The nucleopolyhedroviruses of Rachiplusia ou and Anagrapha falcifera are isolates of the same virus
J. Gen. Virol. 80 (Pt 10), 2793-2798 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harrison, R.L. and Bonning, B.C.
Comparative analysis of the genomes of Rachiplusia ou and Autographa californica multiple nucleopolyhedroviruses J. Gen. Virol. 84 (Pt 7), 1827-1842 (2003)
                                                                        274
                                             CTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGTGT
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AY145471.1 GI:23476465
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AHCMQRAVNMYQDQILQSSKPDELILHFWPDVDKDVFCNPTKQIRAPFSYNHKGTQFS
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QCIKDRFISNGYKIKKVSNRRRVIEVDCNINAAKDIVNNVIIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="AAK85577.1"
db_xref="GI:15213138"
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FAVI CQNGVLITISGSGQFVRQRVANMCAVGGGI FCERRNDCARDRQLIAEALAAS
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80.4%; Pred. No. 4.8e-24;
.ive 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAK85578.1"
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                                                                                                                                                                                                                                                                                                                         /gene="lef-1"
complement (6427. .7182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon start=1
                                                                   codon_start=1
product="unknown"
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                     complement (5531.
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                                                                                                                                                                                                                                                                                                                                                                    gene="lef-1"
                                                                                                                                                                                                                                                                                                                                                                                          note="ORF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497. .10123
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/gene="egt"
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/gene="egt"
7254 .8732
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIVFHKPSSKRDLNSLGALFATKHGLLEILMQLNFANKSNALLHIQTEGERDDLRDKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAPGYGLAENFOTVGAVARHPVYHPNIWRNNFDDTEANVWTEMRLYKEFKILANMSNA
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VKNITLPVINVITQWRHORAVLGHKKWYAFTTQGGLQSSDBALLEAQIPMIGDE
FYHAHKLQQLGVARALDTVTVSSDQLTVAINDMLFNAPIYKKHMAELYALINHDKATF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MLFIIYLVFLRGALCGCALSAFINAHQPKQVIIVPGRSKAKHQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLDKAIKETERVIRYRHDISRQLYSLKTTAANVPYSNYYMYKSVFSIVMNHLTHF"
11578. .11745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYDGVHPNPLLAIQCINEKLYDKHYKIRKIAKRVIDVNCTPNVVKEVIQEVL" complement (9128. . 9931)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCITKELLDKLKQCYPGYGTGGCGPVTTTATTSSPLKIGLIQTTTKSTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 131526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="ecysteroid UDP-glucosyltransferase"
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db_xref="G1:23476484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10045. .11565
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                                                                                                                                                                                                                                                                                                                                                                                          .9239)
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="roll; ac13-like"
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                                                                                                                                                                                                                                                                                                                                                                                          complement (8253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11711, .12388
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Matches 124; Conserv
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DIAVVPVSVR VQNGWQI FERINNFEREI SQDMLDOLQI ILGRFEYFRNGKLIRLSTY
FUNDNINVOGWYNKECVYTYVHRINYQSVPAELAPRISEAVKKFIRLKKSDYDDRLHL
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ASSLCENKILLSQINCESFENDFKHYLDDYNYAFSIIDNSTNVLVAFGLYC"
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NTVVLNRDVLLNILKLANDVFDNKAFMYVDDSEVSRHYNAVVKMKRLVIGVRDPSLRQ
SLYNTIAYIERLLNIGTVNDSEITMLIADFYDLYSNYNIELPLPQALPRSRRPSVVQP
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TEPEPVAPLDDRQQLLEAIRNEKNRTRLRPVKPKTVPETNTILELPTVLPKTFEPKPP
SASPPPPPPPPPPPPPPPPPPPPPNVDLSSAPLPPPLVDLPSEMLPPPAPSLSNVLSELK
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SNAAKEDVRXVQSLFNVFTSSQLYTKNDDEMYTKAHDILNDVEALLQNKTQTNIDKA
RLLLQDLASFVYLSSNPLDSFVIGSRRQPLFETNRNLFYKSIEDLIFKFRYKEAENHL
IFALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
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LQIKGELSYQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFEALDRVYVCDYGLC
KHENSPSVHDGTLEYFSPEKIRHYNYARSFDWYAVGVLTYKLLTGGRHPFEKSEDEML
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/note="consists of 30 bp imperfect palindromes; hrla;
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                                                                                              /codon_start=1
/product="late expression factor -
                                                                                                                                                                                                                                                                                                                                                                                   /note="orf603; ro5; ac7-like"
/codon_start=1
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/product="protein kinase - 1"
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/note="polh; ro6; ac8-like"

/codon_starts1

/product="polyhedrin"

/protein_id="AAN28081.1"

/db_xref="G1:23476534"
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/note="pk-1; ro8; ac10-like"
                           1756. .2388
/note="lef-2; ro4; ac6-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3997. .5625)
/note="orf1629; ro7; ac9"
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/product="ORF1629"
/protein_id="AAN28027.1"
/db_xref="GI:23476480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAN28093.1"
/db_xref="GI:23476546"
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/db_xref="GI:23476522"
                                                                                                                                                              /protein_id="AAN28095.1"
/db_xref="G1:23476548"
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'db_xref="GI:23476507"
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                                                                                                                                                                                                                                                                                                                                                        .3064)
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/product="unknown"
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                                                                                                                                                                                                              PAT 07-MAR-1997
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
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Ayres, M.D., Howard, S.C., Kuzio, J., Lopez-Ferber, M. and Posse
The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus
Virology 202 (2), 586-605 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 133894;
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                                                           CTACTACACTATCAACTTTTTTGCATTACAAAAAGTTCATTTTTGC 120
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Submitted (08-MAR-1999) NCBI, Bethesda, MD 20894, USA
Location/Qualifiers

1. 133894
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Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                  unidentified
unclassified
Bishop,D., Possee,R. and Ayres,M.
Bishop,D., Possee,R. and Ayres,M.
AutoGARAPHA CALIFORNICA COMPLETE GENOME SEQUENCE
AUTOGRAPHA CALIFORNICA CARPORDETE
AUTOGRAPHA CALIFORNICA (GB)
Other publication AU 2897295 960125.
Location/Qualifiers
1. 133894
/organism="unidentified"
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                                                                                                                                                                                                              linear
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                                                                                                                                                                                                              DNA
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/db xref="taxon:32644"
                                                                                                                                                                                                            A48542 133894 bp
Sequence 1 from Patent W09601320.
A48542
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JOURNAL
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L22858/c
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PUBMED
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A48542/c
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KEYWORDS
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KEYWORDS
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1 (bases 1 to 1511)
Krappa, R. and Knebel-Morsdorf, D.
Identification of the very early transcribed baculovirus gene PE-38
91101290
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/codon_start=1
/product=1,immediate-early protein PE-38"
/protein_id="AAA4673.1"
/db_xref="d1:332471"
/db_xref="d1:332471"
/db_xref="d1:332471"
/db_xref="G1:332471"
/db_xref="G1:32471"
/db_
                                                                                                                                                                                                                                               NPHPE38 1511 bp DNA linear VRL 02-AUG-1993
Autographa californica nuclear polyhedrosis virus major early
protein (PB-38) gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Autographa californica nuclear polyhedrosis virus DNA, and CDNA to mRNA, isolated from Spodoptera frugiperda. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1511
/organism="Autographa californica nucleopolyhedrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:46015"
complement(1. .294)
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                                                                                                                                                                                                                                                                                                                                                                                     major early protein PE-18.
Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Autographa californica, nucleopolyhedrovirus
Nucleopolyhedrovirus.
                                                                                                                129881 CTACTACACTTTTTTTGCATTACAAAAAGTTCAT 129841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="immediate-early protein PE-38"
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                                                                                CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGT
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/gene="IE-N"
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1433. 1438
/gene="PE-38"
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/gene="PE-38"
352. .357
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379. 1453
/gene="PE-38"
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Matches 12
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                         RESULT 8
NPHPE38/c
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                                                                                                                                                                                                                                                                                  DEFINITION
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AUTHORS
TITLE
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PUBMED
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/ Jobes "LEF2; 23926 Da primary translation product"
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/ Codon start=1
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/ product=1ate expression factor 2"
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INMPPCTKKILNDLKENNVPRGGMYRKRFILMCYTANNVSCAKCENNCLIKALTHFYN
HDSKCVGENNVHILLIKSQDVYKPPNCQKMKTVDKLCFPAGNCKGLNPICNY"
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/translation="WAVIPRNKQLLADNSIEKGGELFLFNGSYNILESXVNPVLLKNG
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PIKKDIYIYDNKKFTLYDRYIYGYDNNYNMFYEEKNEKERFEEEDDKASSLCENKII
LSQINCESFENDFKYYLSDYNYAFSIIDNTTNVLVAFGLYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5287. .6918)
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/note="synonym: AcOrf-9; Ac-61K; Ac-vp78"
complement (5287. .6918)
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/note="61K; vp78; required for virus replication; 60713 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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NTVVLNRDVLLNILKLANDVFDNKAYMYVDDSEVSRHYNAVVKMKRLVIGVRDPSLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MPDYSYRPTIGRTYVYDNKYYKNLGAVIKNAKRKKHFAEHEIEE
TADPLDNILVELVBEDPELGGKNQKLTLEKEIKNYKPOTMKLYVGWKGKERYRETWTRF
MEDSPPINNDGWNWPYELVVNMRPTRPRENRCYKFLAGHALRCDPDYVHDVIRIVEPEN
VGSNNEYRISLAKKGGGCPIMNLHSEYTNSFEQFIDRVIWENFYKPIVYIGTDSAEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLYNTIAYIERLLNIGTVNDSEITMLIADFYDLYSNYNIELPPPQALPRSRRPSVVQP
AAPAPVPTIVREQTKBEQIIPAAPPPPSSPVPNIPAPPPPPSMSELPPAPPMPTEP
QPAAPLDDRQQLLEAIRNEKNRTRLRPVKPKTAPETSTIVEVPTVLPKETFEPKPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFDCNKFLRSDDMTPVVTTITPKRTADYKITEYVGDVKT1KPSNRPLVESGPLVREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4520. .5257
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/note="synonym: AcOrf-8"
4520. .5257
//gene="AG-PH"
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/note="synonym: AcOrF-7"
complement (3759, .4364)
/gene="Ac-ORF603"
/note="ORF603 peptide; 23612 Da primary translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6917. .7735
/gene="Ac-pk-1"
/note="PK1; 31978 Da primary translation product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="major occlusion body protein"
/protein_id="AAA66638.1"
/db_xref="GI:559077"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EILLEVSLVFKVKEFAPDAPLFTGPAY"
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/gene="Ac-pk-1"
/note="synonym: AcOrf-10"
                                                                                                        /note="synonym: AcOrf-6"
3089. .3721
                                                     3089. .3721
/gene="Ac-lef2"
                                                                                                                                                                gene="Ac-lef2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MPPARWHNYLQCGQVIKDSNLICFKTPLRPELFAYVTSEDVWT
AEQIVKQNPSIGAIIDLTNTSKYYDGVHFLRAGLLYKKIQVPGQTLPPESIVQBFIDT
VKBFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHTLGIAPQEAIDRFEKARGHKIERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="BRO; 37769 Da primary translation product"
/codon_start=1
/product="baculovirus repeated ORF"
/protein_id="AAA66632.1"
/db_xref="G1:559071"
/translation="MARVKIGEFKFGEDTFNLRYVLERDQQVRFVAKDVANSLKYTVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKAIRVHVDNKYKSLFEQTIQNGGPTSNSVVKRGDPLYLÕPHTVLITKSGVIQLIMKS
KLPYAIELQEWLLEEVIPQVLCTGKYDPAIKQREEESKQLVTKLIATFTEHTNALQAV
VAQKTEELVKKQEFIERIVAIKDKQIEAKDLQVTRVMTDLNRMYTGFQETMQKKDEIM
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SEDVORFNETURNDLISACMOINVETYMPNATIDMRKQPNCTYFRICQYCHLBADVPS
PDDHSVYRKICVACGTPLVIDHPLDVFGHTEECVNELLEVQRVNAGGEL"
2779. 3108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKKDAQVTDLVÄKVVDLSDRAVQYPÄDKRKHPVLCVTRDGTTFTAITGQKTYVENQKH
KRNINVANIVVENIRPNPTVDWNNATDRLQAKRSKRSIVLVRWKKRNNLKIG"
complement (2084. .2245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rranslation="MQIKTVLLAFAMFAALNAQHVLAACAETGAVCVHNDECCSGACS
PIFNYCLPQ"
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                                                                                 /standard_name="hr1"
/note="5 copies of 30 bp imperfect palindromic sequence;
the EcoRI site in the first palindrome is at residue 1 of
the linearized genome
                                                                                                                                                                                                                                                                                                                                                                                   Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ^note="CTX; 5590 Da primary translation product"
codon_start=1
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'note="17577 Da primary translation product"
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/note="12435 Da primary translation product"
                                                                                                                                                                                         function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                    /gene="Ac-ptp"
/note="PTP; 19288 Da primary translation
/codon_start=1
/product="protein tyrosine phosphatase"
/protein_id="AAAA6631.1"
/db_xref="GI:559070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="conotoxin-like peptide"
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/db_xref="G1:559072"
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/clone="C6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="AcOrf-4 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="AcOrf-5 peptide"
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/note="synonym: AcOrf-2"
complement(1041..2027)
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db_xref="GI:559073"
                                                                                                                                                                                                                                                                                                 'note="synonym: AcOrf-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: AcOrf-3"
complement(2084. .2245)
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                                                                                                                                                                                                                /rpt_type=dispersed
503. .1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="AcOrf-4"
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                                                                                                                                                                                                                                                                           /gene="Ac-ptp"
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                                                           repeat_region
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FVAPS PQATQTPSPRQTFAAPSPVPAES PQPTRAFPTPEGTLSRGAADE FEYFAGTS V
NGVNLNTTLKPPVPPKPAHLSRPNFMFVGDKVTGNTPPPPNGTS PQPGVNVPPPPVAP
PLNVMPPPPPPNVPPPPLDNLLLDAMMSEPRKGATDRSALFDQI KMGATLKKAQPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPSDLRGDMLNQI RTGATLRKTGRLEDENLGKPKKGREGI LGVLYNTLGSRRGGI DSE
RSDVATSESTGFDESADTRANDKASKELKHAAHLYNFRKDSKLYNI QKVNNSELTKI
LENGPPLLKRSPRTABNUERANAGLYL FROHVTLPKNALDAQPAPELYAADAPQFYVQ
IEDLLFAGRYDDARAFI QAVDAPEDMKLKKPLTVANQLSTRGQ"
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VEDSFPIVNDQEVMDVFLVINLRPTRPNRCYKFLAQHALRWDCDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPIMNIHSEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEE
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KQIETSCKKKKQAEERAESAALKRVELAADRMAMQAKAAPYCADDGRWSTLSQQQLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On or before Oct 8, 2003 this sequence version replaced gi:1117788, gi:2581770, gi:174838, gi:4092491.
Location/Qualifiers
1. .131158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1. .738)
/note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                                              Li,X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and Arif,B.M.
Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                          4 (bases 1 to 131158)
Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.
Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Choristoneura fumiferana defective
nucleopolyhedrovirus"
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Lauzon, H.A.M., Jamieson, P.B., Krell, P.J. and Arif, B.M. Direct Submission
Submitted (20-JUN-2003) Molecular Virology Great Labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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join[129349. 131158,1. .20)
/note="0.8F 149; 1629 capsid Op2/Ac9"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EILIEVSLVFKVKEFAPDAPLFTGPAY
Virus Genes 13 (3), 229-237 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="polyhedrin"
/protein_id="AAQ91696.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF 2; Op5"
                                                                         80268 to 81693)
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                                                                         (bases
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                                                                 /translation="MATTNATLQTLVQFYENCKNVKTRYKIINGRFGKISILSHKPTS
KLYLQKTISAHNFNADEIKYHQLMSDHPNFIKIYFHNGSINNQVIVMDYIDOPDLFFT
KLYLQKTISAHNFNADEIKYHQLMSDHPNFIKIYFHNDIKLBNULYFFALDRYVCDYGLC
KHENSLSYHGCTLEYFSPEKIRHTWHIVSPMYAQYLTYKLLTGGHPFEKSEDEML
DLNSMKRRQQYNDIGVLKHVRNVNARDFVYCLTRYNIDCRLTNYKQIIKHEFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The putative LEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tränslation="MSLAAKLIIYNYYAKYNEVHDVYGESYHHYRIVQEYLSESYVNG
MSCIERDVHANRILKSGSCTPDEAVKNIDAGOBIKSLSHWESTSETMETHDDNVREVLE
QIDAVVPVSVYRVONGIFSLANFEREISQDMLDCLQIILGREYFRENGKLIRIANV
FNPNNDVVGWWYNKFCVVTYVHRIMYRSVPAELVPRLGSAVKKFIRLRKSDYDDRLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY327402 131158 bp DNA circular VRL 08-OCT-2003
Choristoneura fumiferana defective nucleopolyhedrovirus complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESYNCPRVIAEMYGRFCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEKSFPCYRUIK
DFGRQCKDVYKNLKDVFDLLHAHSMSDKDKNSLMDLLCVMDCEIIDVDCFYYIFESFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrett, J.W., Lauzon, H.A., Mercuri, P.S., Krell, P.J., Sohi, S.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CEDEFNPV)
                                                                                                                                                                                                   7747. .7864
//standard_name="hrla"
//note="? Copies of 30 bp imperfect palindromic sequence"
/function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choristoneura fumiferana defective nucleopolyhedrovirus Choristoneura fumiferana defective nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                           complement (7899. .8921)
/gene="AcOrf-11"
/note="40093 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTCGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101.4; DB 1.
Pred. No. 1.2e-20;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY327402 AF068194 U10476 U23422 U78194
AY327402.1 GI:37499238
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="AcOrf-11 peptide"
/protein_id="AAA66641.1"
/db_xref="G1:559080"
                  /protein_id="AAA66640.1"
/db_xref="GI:559079"
                                                                                                                                                                                                                                                                                               /rpt_type=dispersed
complement(7899, .8921)
/gene="AcOrf-11"
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75.4%;
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Best Local S
Matches 126
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AY327402
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125597 TCTACGTTTCGTAGACTATTTAACTTGAATAGTCTACACTGTTGTATACGCTCCCAATAC 125656
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                                                                                 /protein_id="AAQ91663.1"
| Da xref="G1:37499264"
| translation="WXRILIVISEFEALLYIVWPFYQAYQHIQTAQHDYNDTLTDRMD
XIESVWRRRRHYVPMEALPSVQFDTNLGTLAGETLKCMSVPLYVTEIDLPFFDCTQVCE
                                                                                                                                                                                                                                                            TRRFEMRCNARDNNNÄLMFVNPLNPLECLPNVCTNVNYVHTSVRPNFETGECDCGDEA
VTRVRHVVPGDRSSVCASIVDGLDTTTASHRFRVECVNTYTSIGNFSNNKLLCPSDTF
DSNTDAAFAFEVPGSYPLSGNGLDEPTHRFFLDTRSRIRYNDVRGLIN"
                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="actin rearrangement inducing factor"
/protein_id="AAQ91678.1"
/db_xref="GI:3749279"
/translation="MLAQINYILQLVLHAALYTITLIAFVPSLMGTINYKYAFLLELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVYRHDFVKKCVĞCRMEVRHDEPTVFNQNQCALIMMYMMTAVLQFWNMYVQRKEMRYK
PTPVKTLYFESAPLKEQDTADEEBEQQSSFRMLEIISEPRVQFQFPESSSLDRLSSPP
PIVQSSSSPNSPDSGIDYDIPQPFYSVPNKVVCKYLCRTHATLCA"
                                                                                                                                                                                                      DPGASYFFVGEGDTYVVNGHKLAVGGYCTTNSVPRDCNRETSVVLMSLNQWTCIAEDP
RYFAGTSNWTQLAGRQHFDRILPGQSDRNVLFDRLLGREVNVATNTFRRSWDELLEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNGHSVINLSVLTAFLLGPCVFTTTWAIYKFLLCYKRAEMHSNFYMKTIISLAHVMA
LVCWTLFVVFQPQIYKNGHVPVLDARYRDYDRNSLCWSNIVSDTYEVHDTNAIRTDFN
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R Kang, W., Imai, N., Gomi, S. and Matsumoto, S.

A virus in which a gene for controlling an insect behavior is a virus in which a gene for controlling an insect behavior is batent: JP 2003024062-A 3 28-JAN-2003;

THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
OS Bombyx mori nucleopolyhedrovirus
PN JP 2003024062-A/3
PP 10-JUL-20013
PP 201209305
PI WONKYUNG KANG, NORIKO IMAI, SUMIKO GOMI, SHOGO MATSUMOTO PC CIZNIS/09, A01KG7/033, CIZNI/04

CC From 100,001 to 128413 of BmNPV genome DNA
FH Key

FT SOURCE 1. . 28413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A virus in which a gene for controlling an insect behavior is deficient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTAC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 100; DB 14;
Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                   7898. .8863
/note="ORF 11; arif Op19/Ac21"
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/note="ORF 12; Op18/Ac19"
/codon_start=1
      'note="ORF 10; Op20/Ac20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown"
/protein_id="AAQ91753.1"
/db_xref="G1:37499354"
                           /codon_start=1
/product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD187790
BD187790.1 GI:32997529
JP 2003024062-A/3.
unidentified
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illarity 80.6%;
Conservative 0
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Best Local Similarity
Matches 129; Conserv
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BD187790/c
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                                                   /translation="WGSAMMNPAAGYSSLQNSEKYLIDPNDFYGYLALSPCTVFKQGL
FMEMSGLRLRALLTAPKPTEPKRAYLHRSKRNYCLKACADGSVNLAKALNSLRMPLCM
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| Dax xref="GG1:37499381"
| translation="WINPPMPRTANAVIVSNHDYDREQIRRDLNSLRRSVHELCTRST
TGFDCNRILLELSSSSNDVITKSPVIIKNSAATVGQSALVCDKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAQ91737.1"
/db_xref="G1:37499318"
/translation="MASARFIKFSIRVTQGFKENIVADITHLARLRALIDGKVTHTDV
/RRGFLDRRALVEGAVAVVQYYPDGTIRLNPKTIYFRVCQKCHAVADVPAFDDHSI
ARYLCAACGMVLVIDHPLDVFGDTEEGVNELIEVQRINAGGDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAIRTHVDDKYKTSFEQTIQLGGSTSTNLVKRGDPLVLQPHTVLITKSGVIQLIMKSK
LPYAVELQENLLEEVIPQVLCTGKYNPAIKQQDEBKKQLINKLVKTFSDHTWTLQTAL
LQCYQELVKKQSFIERIVAKNQIEBESDHQKKDEINQ
QKDQDLVKXQSFIERIVAKVIDLSGRAVQYPEDERKHPVLCVTRDGTTFFTAIAGQKAY
KNLSAADIVAKVIDLSGRAVQYPEDERKHPVLCVTRDGTTFFTAIAGQKAYVINQKLK
RNLSAADIVAETTRPNPTVDWNNATHRLAAKKSKRTISFDSEQDAQQPATRIKQLLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MYDANQIDENLFVGGYYGNNEAMLQFIKKHDIESVISLIDSDVG
PIRQALGLPAGYHIHVYCEDEPTCMALINAMDALYDYIERRINEGKKILIHCHAGVSR
SATLAVYYWKKWQVSYEKALRFVNNKRNVALSDHFVRFLSSRCTYRFVNNKLKHVG
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DPTIKLDGWWYNKFCVLTYMYRIIRGTVPAELITRLQNVVTKYIKPEYDESNNALAMG
DVYGRFCGIGKDHFAQHKMRSVYIFPQYMRGEVTYADERFPCFSVIKDFGRQCKETYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="WEPGRWHNYTTCGKVIEGTNLICFKVPLKQEVFEVVTNDEDRWT
VSNLVNRQRALGAVIDLTNTLRYYDGAKVRDAGVLYKKIRVPGQEVPNEDIVQEFFDS
VQEFSARCPGMLIGVHCTHGLNRTGYLVCRYIIDKLHVSPTDAIARFEAARGHKIERR
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TSCVRRDIETARRLNRGELSFDDARRQLNLEEIAKRLATWYHTGEMKSFCSEIQSVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation≈"MAQIKIGQFKFGEDVFTLRYVLDRDIVKFVAKDVASSLKYNICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIQLQVDILHSHAMTDKQKNALFDLLCCNNASDIDVDCYDYIVKKFYNIAVY"
                                                                                                                                             EVTHLLIKAEDVYKPSNCAKMKTVNKLCPKAGMCKGKNPICNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4155..4676)
/note="ORF 8; ptp-1 Op10/Ac1"
/codon_start=1
/product="protein tyrosine phosphatase 1"
/protein_id="AAQ9126.1"
/db_xref="GI:37499327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3686, .4168)
/note="ORF 7; ptp-2 Op9"
/codon start=1
/product="protein tyrosine phosphatase 2"
/protein id="AAQ91731.1"
/db_xref="G1:37499332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2647. .3657

/note="ORF 6; bro Ac2"

/codon start==1

/product==baculovirus repeated ORF"

/brotain_id="AA691674.1"

/db_xref="G1:37499275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="unknown"
/protein_id="AAQ91675.1"
/db_xref="GI:37499276"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1935. .5921
/note="ORF 9; Op11/Ac11"
                                                                                                                                                                        complement(1861, .2124)
/note="ORF 4; Op7/Ac5"
                                                                                                                                                                                                                                                                                                                                                                                                         2171. .2608
/note="ORF 5; Op8/Ac4"
protein_id="AAQ91716.
db_xref="GI:37499317"
                                                                                                                                                                                                                                                               product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product = "unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYLEDLLKRHVRR"
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FETLDIKGELSHQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFERLDRVYVCDY
GLCKHENLPSVHDGTLEFFFPEKIRRHNYARSFDWYAVGVLTYKLLTGGRHPFEKSED
EMLDLNSMKRRQQYRDIGVLKHVRNVNARDFVYCLTRYNLDCRLTNYKQIIKHEFLS-
COMPLEMENT (3248. , 4270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNPNSDAVGWYNKFCVITYVHRIMHRSVPAELVPRLSEAVKKFIRLSKSDYDDRLHV
DESYNCPRVIAEMYGRFCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEKSFSCYTVIK
DFGRQCIDVYRDLKDVFDLLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYYIFESFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSHIVKWDSFKCNTHSFKYRYVHNDTNAKFYNVIDFCKGLEIAHDDILDCNWDSDQYY
THIZBIIFHKQKSKRDLNSLGALFATKQGLLKILMRLNFDNSGNALLHLQTEGRRDDLR
DKIESVLKHVKLATNSEKRWTHETFKNDVGNRFEQFELRLNELDAKLNMLQSAEKL
KTAIVTESKUGTVTFPRDITKHQHLAIFSRBIDDRIKLAFVLGQERHFRKRKNRFEDD
MEVLYDGVHPNPLLAIQCINEKLYDKHYKIRKIAKRAKRUDVDCTHNVVKEVIQEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLLLQDLASRVVLSENPLDSPAĪGLQKQPLFETNRNLFYKSIEDLIFKFRYKDAENHL
IFALTYHPKDYKFNELLKYVQQLSVNQQRTESNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MATTTATNATLQTLVQFYENCKNVKTRYK1INGRFGKISILSHK/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC63687.1"
/db_xref="GI:3745840"
/translation="MLSWLWNWWWWSGDNDDDDNDAAIAAEDRFDPDDYKKYHINVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QI DAVVPVSVRVQTGRQI FSLNNFERE I SQDMLGCLQI I LGR FEH FMRNGKLLHI ANV
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/note="31098 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="32442 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Orf_5"
/note="39315 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Orf_4"
/note="397<u>5</u>6 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Protein Kinase=PK1=AcMNPV orf10"
/protein id="AAC63685.1"
/db_xref="GI:3745838"
                                                                                                                                                                                                                                                             EILIEVSLVFKIKEFADDALFTGPAY"
complement (768, .2396)
/gene="orf1629"
complement (768, .2396)
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/db_xref="GI:3745839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="AcMNPV orf13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (3248. .4270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4605. .5600)
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complement (4605. .5600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (5480. .6292)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22231 AATTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATATAATATACAGTACGAACT 22172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    אס בארחוסטר באר 128413 pp DNA circular VRL 05-MAY-1999
Bombyx mori nuclear polyhedrosis virus isolate T3, complete genome.
L33180
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Gomi,S., Majima,K. and Maeda,S.
Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus
J. Gen. Virol. 80 (Pt 5), 1323-1337 (1999)
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/organism='Bombyx mori nucleopolyhedrovirus'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (19-MAX-1994) Department of Entomology, University of
California, Davis, CA 95616, USA
4 (bases 1 to 128413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-0CT-1998) Laboratory of Molecular Entomology and Baculovirology, The Institute of Physical and Chemical Research (RIKEN), Hirosawa 2-1, Wako 351-0198, Japan Sequence update by submitter on Oct 14, 1998 this sequence version replaced gi:1196668.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing of the putative DNA helicase-encoding gene of the mori nuclear polyhedrosis virus and fine-mapping of a region involved in host range expansion (1), 173-179 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
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                                                                                                                                                                                                                                                                                                                                                       Length 28413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 CTACCACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="28817 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleopolyhedrovirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Indels
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                                                                                                                                                                                                                                                                                                                                                           .
9
                                                                                                                                                                                                                                                                                                                                                   Score 93.4; DB 6;
Pred. No. 3.2e-18;
0; Mismatches 46
                                                                                                  1. .28413
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

    .128413
    /organism="Bombyx mori r
/mol type="genomic DNA"
/isolate="T3"

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Bombyx mori nucleopolyhedrovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 128413)
Kamita, S.G. and Maeda, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon start=1
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                                                                                                                                                                                                                                                                                                                                                   16.6%;
ilarity 72.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gomi,
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                     F
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NPHT3COMP/c
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ACCESSION
VERSION
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                                                                  /trānslation="MLLCNYTQKRVDMMDAIAYNDSRKYAFMTVNARWIHADKYFDT
AGDYSYYYONKVSDYHVKRLDDGGGREWVDADYKNYVDBHDLMMLKYYGATAFLLF
YTEBNVSRVMYTGNRGFHLWLKFTDKFKITSAQNVRVHRYKAFBKPAKLDSDCIQPGS
FAHCVREAVRLYIFHMQDSNLDALTLQYWPDVDRDIFCNVNKQIRAPYSYNXKGTKFE
RCITKELLDKLKQCYPGYGIGGCGPVTTTTTTTFPPSPPKIGSIQTTTKSTT"
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7940 .8101
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700ce="6233 Da primary translation product"
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PERKEKVLIIVDGFDSAYIQATFCSISDSVTIVNKFNEKHVMFDGFVRPDDBGTTMPY
VICELYSVDAAVADRKVKDMVNSIENOQTMLKVFINEANYYNKWNMLKGLIYNNNNNE
SVLVNNVVKFIKVDRYNVTKKNNVTKWVPAVNYFTGRQLLTILFIFFKFK"
complement (9387. .10457)
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VKNITLPANVITQNWFNQRAVLRHKKWAAFITQGGLQSSDEALEAGIPWVCLPMMGDQ
FYHAHKLQQLGVARALDTVTVSSDQLLLAINNVLFNASTYKKHMAELYALINNOKATF
PPLDKAIKTERVIRYRHDISRRLYSLKTTAANVPYSNYYMYKSVLSIVMNHIAHF"
7940. .8101.
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LESAQKYERTYTHRNISSKPAAHWKYFGVVRCDNTIRTIGNEKTVRRLAELCTLYNA
EYVFCQARADGDKDRQALASLLTAAFGPRVIVYENSRRFEFINPDEIASGKRLIIKHL
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YTAANYCLEL EMFKOOFDNINVRNILANNQTPDLVVVBAFADYALVEGHLYDPAPVIO
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LLKQQFGPDTPTIEELRNKVQLLLLNNHPIPDNNRPVSBSVQYLGGGHILVKSARPLTR
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/db_xref="G1:3745842"
/translation="MTILCWLALLSTLTAVNAVNILAVPPTPAYSHHIVYKVYIEALA
                                                                                                                                                                                                                                                                                                                   6407. .7927
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/note="5704 Da primary translation product"
/codon_start=1
/product="UDP-Glucosyl Transferase=EGT=AcMNPV orf15"
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/noce="6501 Da primary translation product"
(Codon start=1
/product="BV/ODV-E26=ACMNPV orf16"
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/note="34057 Da primary translation product"
/codon start=1
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/db_xref="GI:3745841"
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/db_xref="GI:3745845"
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/protein_id="AAC63693.1"
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complement (9387. .10457)
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/gene="bv/odv-e26"
8067. .8756
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/gene="Orf_9"
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122172
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/trainiation="MerlinglanggupytttkDIEDRLRDKIVAKAKLAFIKDCFEA
VCENGGLFVLTGGAAVTCHDDDDYSALKCIDFDYYGLGSKKMFCLGTNLQTNLQKCVD
QHYAELDVLTRQIYARNPLWALKCYONGRARLMGOIDLHLARHIKCIKTQYNDEFDLV
RFALQIDITSAYGVDEYTDNCVKITTAPLSFNVFFVNVRIMKRPFNADRCIKNFSLLG
DEYHULVSZLGRVLNDQLMCLLKDIFTNKFDYKIKRRLHHLKRLFANLDAESYNSCVN
DETHWYLYKCONFTINFVKKILDISGPDLGCRKLMRIYLNTDFRGQLPAYLTHYWN
YPHKNLCDQNWRRTNSIFSLY"
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Xie, W.D., Arif, B., Dobos, P. and Krell, P.J.
Identification and analysis of a putative origin of DNA replication in the Choristoneura funiferana multinucleocapsid nuclear
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Qiu, W., tiu, J.J. and Carstens, E.B.
Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
expression in insect cells
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Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Nucleopolyhedrovirus.
1 (bases 1 to 12960) P. and Krell, P.
Identification of bent DNA and ARS fragments in the choristoneura fumiferana nuclear polyhedrosis virus Res. 24 (3), 249-264 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC
                                                                                                                                                                                                                                    16.6%; Score 93.4; DB 14; 72.5%; Pred. No. 4.5e-18; ive 0; Mismatches 46;
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Virology 209 (2), 538-549 (1995)
95297155
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Virology 209 (2), 409-419 (1995)
95297142
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/note="ORF6;Ac2"
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Lappinte, R., Back, D.W., Ding, Q. and Carstens, B.B.
Indentification and molecular characterization of the Choristoneura
Identification and molecular characterization of the Choristoneura
Itemiferana multicapsid nucleopolyhedrovirus genomic region encoding
the regulacory genes pkip, p47, lef-12, and gta
Virology 271 (1), 109-121 (2000)
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GRHKVVPKSKHVQGLESNLQLLVGVSKHGKMAASDQKILELFYRWSSQTGCEMLDDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-MAY-2004) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2002) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carstens, E.B., Liu, J.J. and Dominy, C. Identification and molecular characterization of the baculovirus CEMNPV early genes: ie-1, ie-2 and pe38 Virus Res. 83 (1-2), 13-30 (2002)
                                                                                                                                Liu, J.J. and Carstens, E.B. Identification, molecular cloning, and transcription analysis of the Choristoneura fumiferana nuclear polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 (bases 1 to 129609)
de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
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de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
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de Jong, J. G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
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On May 13, 2004 this sequence version replaced gi:30269978
Location/Qualifiers
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Nucleopolyhedrovirus
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complement (838. .1449)
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Virology 217 (2), 564-572 (1996)
96183379
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Virology 223 (2), 396-400 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori nuclear polyhedrosis virus genes for BmIE-N and BmPE36, partial cds and complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-FEB-1993) Gentaro Yamamoto, Nagoya University Faculty of Agriculture, Dept. of Agricultural Chemistry; Nagoya, Aichi 464-01, Japan (7el:052-781-5111(ex.6238), Fax:052-781-4447) Submitted (18-FEB-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                  CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclectide sequence and transcriptional analysis of an immediate-early gene, PE36, from Bombyx mori nuclear polyhedrosis
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                             16.3%; Score 92.2; DB 14; Length 129609; 78.3%; Pred. No. 1.1e-17;
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/organism="Bombyx mori nucleopolyhedrovirus"
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BMIE-N; BMPE36; immediate-early gene.
Bombyx mori nucleopolyhedrovirus
Bombyx mori nucleopolyhedrovirus
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Nagoya University
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/translation="MPRETNNRRHRSTPYERPTLEDLHRQLEDALERRYQTRRRQRQ NRERRYQTRRRQRQ NRERRYQTRRRQRQ NRERRYQTRRRQRQ NRERRYQTRRERYQTRRRQRQ NRERRYQTRORDANDERPLETCHGGEGFCF NCVIDLOSNAMNI PHESI VCCPLCNTQVKMMRSLKPRANVTCKFYKKTGERVBAVQOYK NIIKVLQERSVISVENNDKNCDINMENQAKIVALEAELKTEKNHSDQVTSENRQLTEE NTKLNEQVQELQRQVRTLRPQRGITVNPQIGRDDSAPAELNERFRSLAYSTISELFIE NRVHSIQNYYYAGTSGAASSCDVNVTVNPGFEN"

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                                                                                                    /protein_id="BAA03364.1"
/db_xref="GI:222186"
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complement (487.
                                                               /codon_start=1
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CL077394 CH216-145
BX147578 Danio rer
CG751412 P045-4-E0
BH517933 BOGBL87TF
NG3322 YZ35H10.81
BZ992838 CH240_18P
BZ899636 CH240_16P
CC34134 AGENCONT
AL063938 DEOSOPHI
A147474 ED34506.x
BI84287 EEFSOFOX
CG385894 MBRAVOSTR
B184287 TETRAGON
CG938994 MBRAVOSTR
BH757407 SALK.0561
AG358704 MBRAVOSTR
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CL510716 SAIL 836
BM278655 As LGZ_65
CL753134 OR BBa012
AG401197 MUS MUSCU
                                                  ; Search time 4071.35 Seconds (without alignments) 5273.001 Million cell updates/sec
                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                               1 catgatgataaacaatgtat.....tgttacagcgacacatg
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      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                   34239544 seqs, 19032134700 residues
                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                  October 24, 2005, 18:41:23;
                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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seq length: 200000000
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99b est2:::

99b est4:::

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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dirrysia;
Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 679)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: Kmita@niaa.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          679 bp mRNA linear EST 05-FEB-200
AV398660 Bombyx mori ovary BmNPV infected; 6 hr after inoculation
Bombyx mori cDNA clone NV060140 T3, mRNA sequence.
AV398660
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/cell_type="mm cultured cell"
/dev_stage="mmVpv infected; 6 hr after inoculation"
/clone_lib="mmVpv mori ovary mnNpv infected; 6 hr after inoculation"
                                                                                                                                                                                                                                   ENTPM01TF
CH213-86H
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                            AL188860 T
AQ751255 H
CG020891 Z
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BM525801 E
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CN755468
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BH150387 E
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CE275017
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CL089685 1
CG578872 0
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                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bombyx mori"
/mol_type="mRNA"
/db_xref="taxon:7091"
/clone="NV060140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bombyx mori (domestic silkworm)
Bombyx mori
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BH150387
CL645025
CE275017
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BG247625
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CNS0067B
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                                       61 TITTATTAGAATAGTCTACACTGTACTATACGCTCTCAATATACTACTACTACAATTTAGAATA
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                                                                                                                                                                                                                                                                                                                        Xenopus tropicalis (western clawed frog)

Europus tropicalis

Europus tropicalis

Europus is detacos; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Chordatae; Xenopus; Silurana.

(bases 1 to 954)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CH216-145B11_Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-145B11, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="texon:8364"
/clone="CH216-145B11"
                                                                                                                         121 Tritificarracaaaaacricarritic 150
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High quality sequence scop: 226.
Location/Qualifiers
1. 954
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Best Local S:
Matches 87,
                                                                                        249
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Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases Lo 762)

Humphray, S. J., Huckle, E. and Durham, J.L.

Direct Submitssion

Submitted (27-5AN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambrished

This sequence was generated from the T7 end of BAC 109J14. 109J14

This sequence was generated from the T7 end of BAC 109J14. 109J14

This part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene, Further details:
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
pacificus
MMI. Genet. Genomics 269 (5), 715-722 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 TACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCG 276
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Max-Planck-Institute for Developmental Biology
Spenannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf. sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Danio rerio"
/mol_type="genomic DNA"
/mol_txef="tenomic DNA"
/db_xref="tenomic DNA"
/clone="DKEY-109114"
/tissue_type="Testis"
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CG751412.1 GI:37973841
BX147578.1 GI:27978953
                                                                  Danio rerio (zebrafish)
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156 ATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGT
   CCAACTITITIGCACTGCAAAAAACACGCTTTTTGCACGCGGGCCCATACTAGTACAAA
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:285091"
                                                                                                                                                                                                                                                                                                                                                N63392.1 GI:1211221
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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Best Local S:
Matches 97
   110
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AUTHORS
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KEYWORDS
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BOGBL87TF BOGB Brassica oleracea genomic clone BOGBL87, genomic
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                                                                                                                                                                                                                                                                                                                               98 GCCTCCCCACCACCACCTTTTTGCACTGCAAAAAAACACGCTTTTGCACGCGGGCCCAT 157
                                                                                                                                                                                                                                                                                                                                                                                                       158 ACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTAT 217
                                                                                                                                                                                                                                                         38 AACAACAATTCTGTTGAACTGTGTTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTG 97
                                                 /db.xerf="taxon:54126"
/db.cref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genemic DNA with EcoRI and cloning into the BAC vector."
                                                                                                                                                                                                                        Gaps
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1272 regaaaaaaacarrrrrccacccccararrrrrrrcccccaaaaacr 1322
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52.1%; Pred. No. 0.95;
cive 0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="BOGB"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11: cdtown@tigr.org
is from a doubled haploid provided by Tom Osborn.
primer: TF
                                                                                                                                                                              Score 39; DB 9; Length 1324;
Pred. No. 0.81;
0; Mismatches 120; Indels
   pacificus"
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="TO1000DH3"
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'clone="BOGBL87"
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BH517933
BH517933.1 GI:17726023
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48.1%;
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Seq primer: TF
Class: sheared ends.
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TIGR
                                                                                                                                                                                                                      111; Conservative
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Brassica oleracea
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Fax: 301-838-0208
                                                                                                                                                                                                   Similarity
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Best Local Similarity
Matches 86; Conserv
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Best Local
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BH517933/c
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Matches
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TITLE
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NG3392 535 bp mRNA linear EST 01-MAR-1996
yz35h10.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:285091 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 533)
1 (bases I to 533)
2 (bases I to 533)
2 (bases, Lonnon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardia, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                   467 CTCTACAAATTAATTAATACGATAAATTAATAAAAAATAATAATAATGTATAAGGTTAATATA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 246.
Location/Qualifiers
5.7 CCAGTTGGTTTGCACTTTACAAGATTAATGATCAGTACTCTCATCAACAAATATTATAAA
                                                         CTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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49.2%; Pred. No. 1.2;
tive 0; Mismatches 100;
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A Cattle found. Comparative has beart with cattle back and minimal Genome Sequence Contact: Harris Lewin
Unpublished (2003)
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewinGuiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by by University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSRESS and AG99-35205-8834 from USDA/NRI (Livestock
Genome Sequencing Initiative)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewkin, H.A. A. Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                                                            252 CATGCTGATCAATGAGGCATAAAGATATAATTGGTTTATAGACACATTTGTTGGAATGTA 193
                                                                                                                                                                             61 TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCACTTTTTT 120
                                                                                                                                                                                                                              192 TTTACCAAGCTTTTAAACACCCACATTTATGTTTTGGGCCTAAATCATCAGCAAATGAATT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                               Gaps
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                            Indels
                            90;
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     Pred. No. 1.4;
0; Mismatches
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/db_xref="taxon:9913"
/clone="CH240_16P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Bos taurus"
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     Local Similarity 55.2%;
tes 74; Conservative (
                                                                                                                                                                                                                                                                             121 GCACTGCAAAAAA 134
                                                                                                                                                                                                                                                                                                                                 132 TCAGCATTAAAAA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos.
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BZ899636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202.34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative) Plate: 23 row: B column: 3 Seq primer: Sp6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                 578 bp DNA linear GSS 12-JUN-2003 CH240 23B3.TJ CHORI-240 Bos taurus genomic clone CH240_23B3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A. A Cattle BAC-ends and Human A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                             ATACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTC 275
                                                                                                                                                                             GGCAGTCACGTAGGCCGGCCTTATCGGGTCGCGTCCTGTCACGTACGAATCACATTATCG 335
                                                                                                                            278 ATTTGCCCAAATTTCACCAGGTTTTACTTAAAAATTCTACTTATGGGTAAATACCAGGC 337
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="CHOR1-240"
/note="Vector: pTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
Hareford bull il Domino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Pieter de Jong"
Genome Sequence
Unpublished (2003)
Other GSSS: CH240_23B3.TV
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217_333_598
Fax: 217_244_5617
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH40_23B3"
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1. 578
/organism="Bos taurus"
                                                                                                                                                                                                                                                                             336 GACCGGACGAGTGTTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ902838
BZ902838.1 GI:31627927
                                                                                                                                                                                                                                                                                                                            398 GACNGGATAAATNATTT 414
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1 (bases 1 to 578)
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                            218
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Best Local Similarity

6.7%; Score 38; DB 8; Length 578;

Query Match

us-09-896-888a-1.rst

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/lab hose="Yper outsat brascupore rip"
//lab hose="Typer outsat brascupore rip"
//lab hose="Typer outsat brascupore lip"
//lote="Organ: embryo; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: Xho! Library was prepared from 50 ug of
total RNA by oligo-dT priming and ANV reverse
transcriptase. After addition of EcoRI linkers and
ECORI-XhoI digestion, the CONA was size selected by
Chromatography on Sepharose CL-4B columns and fractions
containing CDNAs larger than SOO bp were ligated into
ECORI-XhoI-digested lambda ZAPII (UniZAP-XR) and packaged
in vitro Average insert size is 1.4 kb. The original
library contained 6 x 106 recombinants, of which 3 x 106
were amplified and stored at -70 C in SM buffer containing
phagemids used to infect ToploP. References: Science 253,
196-196 and Methods in Molecular Biology 97, S55-574.
Additional sequences from this library have been deposited
under the name Xenopus laevis dorsal blastopore lip.
Library constructed by Bruce Blumberg (University of
Callfornia, Irvine, Department of Developmental and Cell
     126 TTTTTGATGCAATATATTTGCCAAAAAACTCAGCTTTTATTTTCCATTTTAAACAACTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Cancer Institute / NIH
Bidg. 31 Rm10A07 Bethesda, MD 20892
Email: gapbs=r@mail.nih.gov
Tissue Procurement: Blumberg
CDNA Library Preparation: B. Blumberg
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15322 row: j column: 11
High quality sequence stop: 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 669)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                     CO384338 16.00 669 bp mRNA linear EST 30-JUN AGENCOURT 26189343 Blumberg Cho dorsal blastopore lip Xenopus laevis CDNA clone IMAGE:7297357 3′, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="dorsal blastopore lip"
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Xenopus laevis
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:7297357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                               186 CAATATTTACAAGCTGTT 203
                                                                                                                                                                                                                                                                                                                                                                    CO384338.1 GI:49490161
                                                          235 CCACACATTGAACCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="poth"
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CO384338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEST NISC ROLOGO NEW TINEAR EST 24-MAR-2003 NISC ROLOGO NISC COLOGO NISC COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776553 3', mRNA sequence.
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/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
/note="Vector: pamP1; cDNA prime of pamP1. Size
selected for insert sizes ranging from 0.2-1.8 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
University) or visit the COGENE website at
http://hg.wustl.edu/COGENE website at
                                                                                                         61 TITTCATGITTGCCAACAAGCACCITTATACTCGGTGGCCTCCCCACCACCAACTTTTT 120
                                                                                                                                                                                                                     325 Triraccaagcrittraaacaccacarritargrittraggccraaarcarcagaaargaarr 384
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (Dases 1 to 425)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1977)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation:
                                                       1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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llarity 54.3%; Pred. No. 2.3;
Conservative 0; Mismatches 63; Indels (
  60; Indels
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/dev stage="6 weeks postconception"
lab_host="DH108"
0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:5776553"
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74; Conservative
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Danio rerio (zebrafish)
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                                                                                                                                                                                                 Danio rerio
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Direct Submission

Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and Marmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                           GSS 03-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AACACGCTTTTGCACGCGGCCCATACATAGTACAAACTCTACGTTTCGTAGACTATTTT 192
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CCCATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGT 212
                                                                                                                                                                                                                                                                                                     CNS0039X 1101 bp DNA linear GSS 03-JUN-15
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR08012 of RPCI-98 library from Drosophila melanogaster (fruit
                                                104 ccaataaataggggaacctrcrggraragragaaagaatacarccaargrargcaacgr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                          TGTATACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAA 266
                                                                                                                                                              rdragrcrcagaarracarrrraarcrrrrrrrrrrrrcrrrrcagaaara 217
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clore="BACR08012"
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Similarity 35.9%; Pred. No. 3.9;
11; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           fly), genomic survey sequence. AL063938
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/note="end : T7"
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Jab host="XL1-blue MRF"

/clone lib="Zebrafish WashU MPIMG EST"

/clone lib="Zebrafish liste libority list

/clone lib="Zebrafish list

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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@sresgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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                                                                           EST Danio rerio cDNA clone
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       linear
       mRNA
432 bp
fb34b06.x1 Zebrafish WashU MPIMG
MAGE:3713747 3', mRNA sequence.
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/mol_type="mRNA"
/db xref="taxon:7955"
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Gaps

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HTC 19-AUG-2004

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BI843287

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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CB484581 480 bp mRNA linear EST 01-APR-2003 ccluwtbh009074 Coregonus clupeaformis head Coregonus clupeaformis cDAA, mRNA sequence.
CB484581 GI:29295807
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(bases 1 to 1048)
                                                                                                                                                                                                87 AGTGAACAATTTACAAATATATAAAACAACAACTGTTTTCTGTTGCTACTAAGCACTT 146
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Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

(E-mail : sequences are based on single pass reads.

More information available at

http://www.genoscope.cns.fr/tetraodon.
                                                      27 ATCACTITATITICCTACTGTACAGCGTGAATTITITACTTTTGCAAAGTGACAAAACTG
                                                                                                                                                  169 ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAT
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                                                                                                                                                                                                                                                    229 ACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGCA 279
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     84; Indels
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Tetraodon nigroviridis
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     Mismatches
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Pred. No. 4.5;
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/db_xref="taxon:99883"
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  Conservative
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     87;
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L. Unpublished (1998)

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stagge="4-5 month"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Gong zebrafish voary"
/clone="Dip="Gong zebrafish voary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the Ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                                                EST 04-OCT-2001
                                                                          169 ACTCTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAAT 228
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Please contact Zhyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
                                                                                                                        81 AGTGAACAATTTACAAATATATAAACAACAACTGTTTTCTGTTGGCTACTAAGCACTT
                                                                                                                                                                         229 ACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGCA 279
                                                                                                                                                                                                                     141 ACTCTACTACACATTACACGGAGAGCCTAAAAGTACATGACAAAA 191
                                                                                                                                                                                                                                                                                                                       ft59f05.x1 Gong zebrafish ovary Danio rerio cDNA clone
IMAGE:5157656 3', mRNA sequence.
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50.9%; Pred. No. 3.9;
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/organism="Danio rerio"
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Location/Qualifiers
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/clone="IMAGE:5157656"
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TITLE JOURNAL

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Coregonus clupeaformis
Coregonus clupeaformis
Eukaryotas Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Salmoniformes; Salmonidae; Coregonus.
Protacanthopterygii; Salmoniformes; Salmonidae; Coregonus.
1 (bases 1 to 480)
GRASP Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA libraries
Unpublished (2002)
Contact: Koop BF
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                                                                                                                                                                                                                                                                                                                                 Centre for more control Research University of Victoria BC, VBW 3NS, Canada PO Box 3020 STN CSC, Victoria BC, VBW 3NS, Canada Tel 250 472 4075

Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
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/organism="Coregonus clupeaformis"
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Kristian R von Schalburg ; Lake whitefish tissue
contributor: Louis Bernatchez (Universite Laval)"
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Score Much Length Discore		ID	AAV62487	ADQ48575	AAL61306	ADQ48539	AAT13730	AAT13635	ADC51646	ADQ48576	ABZ10059	AAS46501	ADE84121	ABZ10205	ADE84197	ADA71938	ABQ68715	ABQ70339	AAV34232	ACD08103	ABL19380	AAS18541
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ALIGNMENTS

Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins. This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells Orgyia pseudotsugata; multicapsid; nucleopolyhedrosis virus; OpMNPV; Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bleomycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; ss. pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter. Hegedus DD; Grigliatti TA, Theilmann DA, Pfeifer TA, Orgyia pseudotsugata; polyhedrosis virus. Claim 10; Page 82; 121pp; English. ВР (UYBR-) UNIV BRITISH COLUMBIA. 97US-0049946P. 98CA-02221819. 98WO-CA000282 AAV62487 standard; DNA; 564 (revised)
(first entry) WPI; 1998-557129/47. 26-MAR-1998; 27-MAR-1997; 28-JAN-1998; WO9844141-A2 08-OCT-1998. 17-OCT-2003 19-JAN-1999 AAV62487; RESULT 1 AAV62487 THE STATE OF THE S

replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; OpIB2 promoter.

18-JUL-2003; 2003WO-US022437

WO2004009768-A2 Unidentified

29-JAN-2004

viral vector; recombination site; recombinant virus;

OpIE2 promoter DNA sequence

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that comprises: (i) prokaryotic origin of replication, (ii) insect promoter having homology to, and capable of functioning as, an immediate early baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/phleomycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) calls with heterologous DNA, beterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous
                                                                                                                                                                                             melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell lines from disparate species, allowing screening of lines for optimum post-translational modification of particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise os
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                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 564; DB 2; I 100.0%; Pred. No. 1.1e-172;
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Matches 564; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
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100.0%; Pred. No. 1.8e-167;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 16; 555pp; English
                                                                                                                                                                                                                                 18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-039647PP.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
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Best Local Similarity 100."
Matches 548; Conservative
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                                                                                                                                                                                                                                                                                                                                            BENNETT R P. WELCH P J. HARWOOD S.
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                                                                                                                                                                                                                                                                                                                                                                                          MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sennett RP,
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ADQ48575 standard; DNA; 560

RESULT 2 ADQ48575

(first entry)

09-SEP-2004

ADQ48575;

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                                                                GTCCCGCTTATCGCCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 540
GACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 420
                                                                                                              365 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 424
                                                                                                                                        GGACGCGCCTCCATATCAGCCGCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 480
                                                                                                                                                 425 GGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 484
                                                                                                                                                                                     485 GTCCCGCTTATCGCGCCTATAAAATACAGCCCGCAACGATCTGGTAAAACACAGTTGAACAG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                      Multimeric protein; interleukin 5; IL5; TNPalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouritsen S;
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                                                                                                                                                                                                                                                                                                                                     p2ZOp2F expression vector for insect cells.
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                                                                                                                                                                                                                                                                               AAL61306 standard; DNA; 2773 BP
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16-NOV-2001; 2001US-0331575P.
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NIELSEN F S.
BRATT T.
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viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                            185 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACACACA
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gene therapy. The present sequence is p2ZOp2F expression vector insect cells. This sequence is used to illustrate the method of invention
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                                                                                                                                                                     Length 2773;
                                                                                                             Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
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100.0%; Pred. No. 3.8e-167;
tive 0; Mismatches 0;
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                                                                                                                                                                                               Best Local Similarity 100.
Matches 548; Conservative
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421 GGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                  CATCTGTT
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AAT13730/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention replication of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is useful for constructing a preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that was used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITICATGITIGCCAACAAGCACCTITIAIACTCGGIGGCCTCCCCACCACCATTITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTAGACTATTTTACATAAATAGTCTACACGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardardaraacaargrardgrecraargriccricaacaacaarrcrardaacrere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.9%; Score 546.4; DB 12; Length 5038; 99.8%; Pred. No. 1.7e-166; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             Frimpong K,
                                                                                                                                                                                                                                                                                             Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 18; Page 395-403; 555pp; English.
                                                                                                                                                                                                                                                                                             Harwood S,
2002US-0396335P.
2002US-0398617P.
2002US-0427231P.
2003US-0456496P.
                                                                                  03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 99.8
547; Conservative
                                                                                                                           INVITROGEN CORP.
                                                                                                                                                                                                                                                                                          Bennett RP, Welch PJ,
                                                                                                                                            BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                                                                                                                        MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                    WPI; 2004-132944/13
18-JUL-2002;
26-JUL-2002;
19-NOV-2002;
24-MAR-2003;
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                                                                                                                           (-IANI)
                                                                                                                                                                                                           (MADD/)
(FRIM/)
                                                                                                                                            (BENN/)
                                                                                                                                                                                                                                                 (FRAN/)
                                                                                                                                                                                     (HARW/)
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  BARARA BA
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AAT13636-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-99, 101-103, 106-127, 129-130, 140-140, 148-150, 152 and 154 from a total of 154 ORFs identified in the class of the constant of the second of the constant of the left end of the linear map, and irrespective of its orientation. The direction of transcription is relative to that of the polyhedrin gene. Of the 154 ORFs identified it was found that some of the ORFs (ORFs Teplication in cell culture or insect larvae. These genes can be deleted from the genome to: (a) provide additional sites for inserting single or multiple copies of foreign genes; and (b) to reduce the size of the virus complementary strand relative to the polyhedrin gene. The present complementary strand relative to the polyhedrin gene; The present cequence is designated ORF 152, and is on the complementary strand calculation of the polyhedrin gene. (Updated on 16-0CT-2003 to standardise
                           480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector;
                                                                                                                                                                                             481 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAACACAGTTGAACAG
421 GGACGCCCTCCATATCAGCCGCGCTTATCTCATGCACGTGACCGGACACGAGGCGCCC
                                                                                                                                           GTCCCGCTTATCGCGCCCTATAAATACAGCCCGCAACGATCTGGTAAAACACACAGGTTGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence - useful in the prodn. of vectors for enhanced heterologous protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number= ORF 152
/note= "corresponds to AcNPV nucleotides complement
(132387-132109)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autographa californica nuclear polyhedrosis virus complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Autographa californica nucleopolyhedrovirus; clone 6.
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Gaps

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Indels

Length 133894;

DB 2; 41; 231

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132384 AATTTTTTGCAAAGAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT 132325
                                                                                                                                                                                                                        132324 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 132265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22171 CTACAAATGGTAGACTATTTTATTAGAATAGTCTACACTGTACTATAGGCTCTCAATATA 22112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a Bombyx mori (silk worm) polyhedrosis virus in which open reading frame 8 (ORF 8) gene is inactivated. The inactivated orfs gene is useful for suppressing movement of silkworm and efficiently prevents the movement of a silkworm from a chamber in which it is raised. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel Bombyx mori polyhedrosis virus in which open reading frame gene is inactivated, or its variant, useful for suppressing movement of Bombyx
                                                                                         CTACGTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22231 AATTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATATAATATACAGTACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28413 BP; 8394 A; 5713 C; 5940 G; 8366 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              132264 CTACTACACTATCAACTTTTTTTGCATTACAAAAAAGTTCATTTTTGC 132218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 28413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTCGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAAGTACGTGGGG 278
                       Pred. No. 4.4e-21;
0, Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.6%; Score 93.4; DB 10
llarity 72.5%; Pred. No. 8.6e-19;
Conservative 0; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BmNPV genomic DNA nucleotides 100001-128413
    Score 101.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; silkworm; silkworm movement supression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bombyx mori nuclear polyhedrosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; SEQ ID NO 3; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                          ADC51646 standard; DNA; 28413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-2001; 2001JP-00209305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUL-2001; 2001JP-00209305
    18.0%;
                           75.48;
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-516415/49.
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                         Similarity
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                         Best Local Simi
Matches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2003
                                                                                                                                                                            172 (
                                                                                                                                                                                                                                                                    232 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC51646;
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
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                                                                                                                                                                                                                                                                                           CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector; baculovirus; ss.
                                                                                                                                                                        276 AATTTTTTTGCAATGCAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Autographa californica nuclear polyhedrosis virus complete genome sequence - useful in the prodn. of vectors for enhanced heterologous protein expression, such as interleukin(s), interferon(s) and
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                                                                                                                                 .
0
                                                                                       DB 2; Length 279;
                                                                                                                                                                                                                                                                                                                                                       CTACCACACTTGGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGC 278
                                                                                                                                                                                                                                                                                                                                                                              CTACTACACTATCAACTTTTTGCATTACAAAAAAGTTCATTTTTGC 110
                                                                                   Score 101.4; DB 2; Length
Pred. No. 2.5e-22;
0; Mismatches 41; Indels
                                         BP; 88 A; 36 C; 68 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autographa californica nucleopolyhedrovirus; clone 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 90-186; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT13635/c
ID AAT13635 standard; DNA; 133894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possee R, Ayres M;
                                                                                ucn 18.0%;
al Similarity 75.4%;
126; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-IB000578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACNPV genomic DNA clone 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-087670/09.
                                         Sequence 279
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03-SEP-1996
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ABZ10059 standard; DNA; 6289 BP

ABZ10059;

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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention replication-defective particles, preventing/thibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producting and expressing fusion polypoptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                      viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harwood S, Madden K, Frimpong K, Franke KE;
                                                                                                                                      Viral vector-related plasmid pIB/V5-His-DEST recombination region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 62; DB 12; Length 141; 100.0%; Pred. No. 1.2e-09;
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                                  ADQ48576 standard; DNA; 141 BP.
                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2002; 2002US-039B617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                               18-JUL-2003; 2003WO-US022437.
                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2002; 2002US-0396335P.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bennett RP, Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-132944/13
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                                                                                                      09-SEP-2004
                                                                                                                                                                                                                                           Jnidentified
                                                                                                                                                                                                                                                                                                             29-JAN-2004
                                                                    ADQ48576;
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RESULT 8
                 ADQ48576
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differentiating between healthy heamatopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related by used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferation can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T, Pelet C;
                                                                                                        Haematopoietic cell proliferation disorder related DNA sequence #199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          differentiating between hematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZO9861 to ABZ10118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                              Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.0%; Score 39.6; DB 8; Length 6289; 53.2%; Pred. No. 0.14; Live 0; Mismatches 74; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a method for detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P, Grabs (
Model F, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guetig D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 28; SEQ ID NO 199; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adorjan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2001; 2001US-0278333P.
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 53.28
Matches 84; Conservative
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                                                                                                                                                                                                                                             Homo sapiens.
                                                              16-JAN-2003
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CTTATCGCGCCTATAAATACAGCCCGCAACGCTCTGGTAAAACACACAGTTGAGCATCTG 487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single conjective probes for detecting the cytosine methylation state and/or single conjective probes can also be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or proposition to specific diseases, by analysing claeases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of cytosine methylations. The parameters which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences cervice and/or epigenesic parameters, which are disadvantageous to patients. The present did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
4896 AATTTATATATAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837
                                                                                                           4836 ТААТААТТТТТААААСАТТАТТАТАААААТССТСАСААТТСТТТТТАСТССААААТА 4777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              umour suppressor gene; oncogene; antitumour; cytostatic; cancer; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                   172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor gene derived chemically modified sequence #223.
                                                                                                                                                                                           4776 ATACAACTTTCCTCCCTATAAAAACGAAAAAATA 4739
                                                                                                                                                   232 CTACCACACTTGAACCTTTTGCAGTGCAAAAAGTA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 223; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01013173.
30-JUN-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                    AAS46501 standard; DNA; 9289
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                                                                                                                                                                                                                  7836 TAATAATTITTAAAACATTATTATAAAAATCGTCACAATTCTTTTTACTCAAAAAAA 7777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one spee and/or their regulatory regions in a subject by contacting at least uncleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between methylated and non-methylated CpG dinucleotides within the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MNRL, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2B, FOS, GSK3Deta, ESR1, APPAT1, BAK1, BAX or HOXAS. Oligomers, peptide nucleic acid (PMA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the
                                                                                                          172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least on reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; single nucleotide polymorphism; SNP; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leuxemia; small lymphocytic lymphoma; follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nimmrich I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lymphoid cell proliferative disorder gene derived DNA #57.
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Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
                                  Length 9289;
                                                                     Indels
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                                                                                                                                                                                                                                                                                            7776 Afacaactrrccrcrcccraraaaaacgaaaaaaaa 7739
                                                                     74;
                                  DB 4;
                                                                                                                                                                                                                                                         232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA
                                Score 39.6; DB
Pred. No. 0.16;
                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         ADE84121 standard; DNA; 9289 BP
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                                7.0%;
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28-DEC-2001; 2001DE-01064501.
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                                                                     84; Conservative
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                                                      Local Similarity
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7836 TAATAATTTTTAAAACATTATTATAAAAATGGTCACAATTCTTTTTACTCAAAAAATA 7777
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CpG dinucleotides within one or more the sequences, or their complements, for determining the cytosine methylation state and or single nucleotide polymorphisms (SNPs), and for differentiating at least two of the medical conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular lymphoma. They are also useful for detecting of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence represents a nucleic acid of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                              172 CTACGTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                             Score 39.6; DB 10; Length 9289;
Pred. No. 0.16;
0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                          Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                           74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269
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                                                                                                                                                                                                                                 above mentioned genes.
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Best Local &
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Haematopoietic cell proliferation disorder related DNA sequence #345. 205/c ABZ10205 standard; DNA; 6289 (first entry) 16-JAN-2003 ABZ10205; RESULT 12 ABZ10205,

Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.

Homo sapiens

WO200277272-A2

03-OCT-2002.

26-MAR-2002; 2002WO-EP003401.

26-MAR-2001; 2001US-0278333P.

(EPIG-) EPIGENOMICS AG.

Pelet C; Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T, , Braun A, Distler J, Guetig D, Piepenbrock C, Adorjan P, Grabs Lipscher E, Maier S, Model F, Lipscher E, I Ziebarth H; Olek A, Pie Lewin A, Li Schwope I, Berlin K,

WPI; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 28; SEQ ID NO 345; 117pp; English.

The present invention describes a method for detecting and differentiating between hacmatopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a

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biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the trarget nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative discorder haematopoietic cells in an proliferative discorder haematopoietic cells in an proliferative lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related polymorphisms (SNPs) of haematopoietic cell proliferation disorder related camplification of haematopoietic cell proliferation between sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferation of patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphoid cell proliferative disorder gene derived DNA #133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6289 BP; 1680 A; 0 C; 1488 G; 3121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.7%; Score 38; DB 8; Length 6289; 52.5%; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytic leukemia; small lymphocytic lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4776 aracaacrincerereceraraaaacaaaaaaaaa 4739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     follicular lymphoma; diagnosis; prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genc B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE84197 standard; DNA; 9289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-2002; 2002WO-EP013265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-457621/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003044226-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2003
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ADE84197/c
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The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least cone gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with car least one reagent or series of reagents that distinguish between methylated and non-methylated Sample obtained from the subject with car least one reagent or series of reagents that distinguish between condition. The genes and/or their regulatory regions are preferably selected acid. The genes and/or their regulatory regions are preferably selected from MDRI, CSNK2B, EGR4, AR, CDK4, RB2, CDC5A, GPID beta, MYDDI, CDR3, CK GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TGFN2B, CDKNIC, CGSKDeta, ESR1, APAF1, BAK, BAX or HOXAS. Oligomers, peptide nucleic acid (SKNbeta, ESR1, APAF1, BAX, BAX or HOXAS. Oligomers, peptide nucleic acid (SKNbeta, ESR1, APAF1, BAX, BAX or HOXAS. Oligomers, peptide nucleic of the genes are useful for detecting the methylation state of all the conditions such as diffuse large Barel and or single nucleotide polymorphisms (SNPs), and for differentiating and least two of the medical conditions such as diffuse large Barel and or single nucleotide lamphoon, Tymphoma, They are also useful for detecting of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treating and/or above mantioned from the prove mentioned of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AACTITITIGCACTGCAAAAAACACGCTTTTGCACGCGCCCATACATAGTACAAACT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 CTAÇGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; bacterial infection; fungal infection; viral infection; rice;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.7%; Score 38; DB 10; Length 92
Best Local Similarity 52.5%; Pred. No. 0.54;
Matches 83; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA
                                                               Claim 26; SEQ ID NO 193; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003000898=A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
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involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a murant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 WARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYCGCSYCGSSKWKY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 MSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCKKY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 CGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                      Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 CYGCKAWTYCSYGYMKWYTYMGSYKYSRCYKYMRMYMYKGWMYMMYYSAYSSMMTWYYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 AKYWKYWYKRRGIMSWYGKSYKKKYC--IWWCYMKCMRCWRCYRWRKMMRKKTKYSKRCYCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 RYATCYWCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSYYMSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 TCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 CTGCAAAAAACGCCTTTTGCACGCGGCCCCATACATAGTACAAACTCTACGTTTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 AGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                 present invention relates to a method (M1) for identifying genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; Listeria; food contamination; mutational analysis;
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                   Zon
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 Hon Y;
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SA, Hou
Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.4%; Score 36.2; DB 8; Length 20 Best Local Similarity 11.3%; Pred. No. 1; Matches 42; Conservative 169; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes 4b contig DNA sequence #1481.
Goff
               Xie Z,
Glazebrook J,
Whitham S, Xi
                                                                                                                                                                                  Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes ATCC 19115.
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Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSSTSRWMSM 63
Chang H, Chen W, Co
Katagiri F, Quan S,
                                                     WPI; 2003-175290/17.
                                                                                                                                              gene expression.
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29-AUG-2002
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The present invention relates to nucleic acid sequences (AB067188-AB071212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                 New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Score 35.4; DB 6; Length 986; illarity 56.4%; Pred. No. 1.3; Conservative 0; Mismatches 51; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 986 BP; 295 A; 199 C; 157 G; 328 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; SEQ ID NO 1528; 180pp; French.
                                                                                                                                                                               (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                   04-OCT-2001; 2001WO-FR003061.
                                                                                                                                             04-OCT-2000; 2000FR-00012697.
                                                                                                                                                                                                                                                                                          WPI; 2002-332479/37
                                                                                                                                                                                                                                                 Kunst F, Glaser P;
                   WO200228891-A2
                                                            11-APR-2002
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318 CAGATTTAGAAAACATTTATCGTTGCCCAGGAAATTTAAATATCAAGAGCACTCTGTTG 259 258 CAGAACATTCATATAAAGTTACATCCATTGCTCAATTTTTCGGTGCTGTAGAAG 202 215 TATACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACG 271 g ò

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0; Gaps

155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGGTTG 214

Similarity

Local Sim.

Query Match Best Loca Matches Search completed: October 24, 2005, 18:57:59 Job time : 624.051 secs

Sequence 127, App Sequence 127, App Sequence 16, Appl Sequence 199, Appl Sequence 223, App Sequence 1528, App Sequence 315, App Sequence 315, App Sequence 39, Appl Sequence 39, Appl Sequence 2611, Appl Sequence 2611, Appl Sequence 2611, Appl Sequence 2178, Appl Sequence 2178, Appl Sequence 2178, Appl Sequence 6451, Appl Sequence 6451, Appl Sequence 1163, Appl Sequence 1640, Appl

Sequence 2215, App Sequence 127, App Sequence 914, App Sequence 580, App Sequence 5148, Ap Sequence 5148, Ap

Sequence 493597,

Sequence Sequence Sequence

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1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATACTGTTGAACTGTG
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1 US-10-622-088-89

US-09-86-888A-14

US-09-86-888A-14

US-09-86-888A-16

US-00-912-115-199

US-00-911-86-89

US-00-911-89-89

US-09-91-85-89

US-09-91-85-89

US-09-91-86-89

US-09-91-86-89

US-09-91-166-91-86

US-11-060-756-6179

US-09-925-065A-68947

US-09-925-065A-68947

US-09-925-065A-125

US-09-938-842A-5148

US-09-938-842A-5148
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ORGANISM: (
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Sequence 126, App
Sequence 60, Appl
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Sequence 60, Appl
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_PUBW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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                                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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1 US-10-622-088-126

7 US-10-295-074-60

US-10-846-911-60

4 US-10-939-107-60
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Maximum Match 100%
Listing first 45 summaries
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                                                TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCACTTTTTT
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APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Steven
APPLICANT: Madden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OB INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-07-3
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Publication No. US20040219516A1
GENERAL INFORMATION:
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                                                       Length 560;
                                                                                                                            1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCT
                                                                                         Indels
                                                   Query Match 97.2%; Score 548; DB 21; L
Best Local Similarity 100.0%; Pred. No. 6.3e-170;
Matches 548; Conservative 0; Mismatches 0;
; OTHER INFORMATION: OPIE2 promoter sequence US-10-622-088-126
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OTHER INFORMATION: HindIII site
FEATURE:
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485 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAAACACAGTTGAACAG 544
                                                     421 GGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 480
365 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 424
                                                                                                                                                              481 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
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APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: MIELSEN, Finn Stausholm
APPLICANT: BATT, Tomas
APPLICANT: BATT, Tomas
APPLICANT: BATT, Tomas
APPLICANT: MOURITSEN, Soren
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: 674542-2018
FILE REFERENCE: 674542-2018
CURRENT APPLICATION NUMBER: US/10/846,911
CURRENT FILING DATE: 2004-05-14
PRIOR PELING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: FO/331,575
PRIOR APPLICATION NUMBER: PA 2001 01702
PRIOR FILING DATE: 2001-11-16
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NAME/KEY: misc_recomb
LOCATION: (561). (566)
OTHER INFORMATION: HindIII site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial sequence
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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OTHER INFORMATION: Aval site
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LOCATION: (625). (630)
OTHER INFORMATION: ClaI site
FEATURE:
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OTHER INFORMATION: BamHI
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LOCATION: (586)..(591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                               FEATURE:
NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
                                             NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_recomb
LOCATION: (1156). (1161)
OTHER INFORMATION: Apall site
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LOCATION: (2551).. (2556)
1 THER INFORMATION: ApaLI site
US-10-295-074-60
                                                                                                                                                                                                                                                                 NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
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NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
OTHER INFORMATION: Aval site
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TYPE: DNA
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100.0%; Pred. No. 1.4e-169;
tive 0; Mismatches 0;
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NAME/KEY: misc_recomb
LCOARION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                  NAME/KEY: misc_recomb

LOCATION: (2551).. (2556)

OTHER INFORMATION: Apall site

US-10-846-911-60
LOCATION: (2128)..(2133)
OTHER INFORMATION: PStI site
FEATURE:
                                           FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)...(2209)
OTHER INFORMATION: Ncol site
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NAME/KEY: misc recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.
Matches 548; Conservative
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APPLICANT: Rasmussen, Peter Birk
TITLE OF INVENTION: NOVEL Application of Vaccination Against TNF-alpha
FILE REFERENCE: 674542-2020
CURRENT APPLICATION NUMBER: US/10/939,107
CURRENT FILING BATE: 2004-09-10
PRIOR PILING BATE: 2004-09-11
PRIOR FILING DATE: 2003-03-11
PRIOR FILING DATE: 2003-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 60
SOFTWARE PATENTIAL VEFSION 3.1
SEQ ID NO 60
LENGTH: 2773
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LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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NAME/KEY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apali site
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LOCATION: (2551)..(2556)
OTHER INFORMATION: ApaLI site
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence FEATURE:
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OTHER INFORMATION: BamHI site
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (625)..(630)
OTHER INFORMATION: Cla1 site
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OTHER INFORMATION: ClaI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: Pstl site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG

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Sequence 60, Application US/10939107
Publication No. US20050180947A1
GENERAL INFORMATION:
PAPLICANT: Pedersen, Hans Rudolf
APPLICANT: Ebert, Bjarke
APPLICANT: Pedersen, Louise Henriette

APPLICANT:

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                                             GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC 240
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Sequence 89, Application US/10622088

Publication No. US20040219516A1

GENERAL INFORMATION:
APPLICANT: Bennett, Robert P.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Primpong, Kenneth
PRICANT: Primpong, Kenneth
PRICANT: Primpong, Kenneth
PRICANT: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PLING DATE: 2002-07-18
PRIOR PPLING DATE: 2002-07-18
PRIOR PPLING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR PPLICATION NUMBER: US 60/456,496
PRIOR PPLING DATE: 2003-01-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR PPLING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR PLING DATE: 2003-03-03
NUMBER OF SEO ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEO ID NO 89
LENGTH: 5038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                      Gaps
                                                                                    Query Match 96.9%; Score 546.4; DB 21; Length 5038; Best Local Similarity 99.8%; Pred. No. 6.3e-169; Matches 547; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Promoter
OTHER INFORMATION: sequence of the OpMNPV ie2 gene
US-09-896-888A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/0989688A
Fatent No. US20020116723A1
GENERAL INFORMATION:
FILE OF INVENTION: Insect Expression Vectors
FILE OF INVENTION: Insect Expression Vectors
FILE REFRENCE: 80021-44
CURRENT APPLICATION UNMBER: US/09/896,888A
CURRENT FILING DATE: 1908-03-26
FRIOR APPLICATION NUMBER: 06/049,946
FRIOR APPLICATION NUMBER: 60/049,946
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1997-03-27
FRIOR FILING DATE: 1997-03-27
FRIOR FILING DATE: 1997-03-27
FRIOR FILING DATE: 1907-03-27
; OTHER INFORMATION: pIB/V5-His-DEST
US-10-622-088-89
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OTHER INFORMATION: Recombination region of
  NAME/KEY: misc_feature

| LOCATION: (141) .. (148)

| OTHER INFORMATION: n may be any nucleotide

US-10-622-088-127
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Publication No. US20040219516A1
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LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c, g,
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APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
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; LOCATION: (145)..(276)
US-10-622-088-149
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US-10-622-088-149
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                                                                                                             102 CCCCACCACCATITITIGCACTGCAAAAAAACACGCTTTTGCACGCGGGCCCATACAT 161
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                                                                                                                                                          1 cccaccaccarrrrrrgcacrgcaaaaaaacacgcrrrrrgcacgcgcccaracar
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                                                        Gaps
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Publication No. US20040219516A1
GENERAL INCORMATION:
APPLICANT: Bennet. Robert P.
APPLICANT: Walch, Peter J.
APPLICANT: Madden, Knuch B.
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: US/10/622,088
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: PCT/US03/22437
PRIOR PLING DATE: 2003-07-18
PRIOR PLING DATE: 2003-07-18
PRIOR PLING DATE: 2003-07-18
PRIOR PLING DATE: 2002-07-18
PRIOR PLING DATE: 2002-07-18
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2003-07-18
PRIOR PLING DATE: 2003-11-19
                                                        .;
0
Query Match 81.9%; Score 462; DB 9; Length 462; Best Local Similarity 100.0%; Pred. No. 1.5e-141; Matches 462; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
FEATURE:
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ORGANISM: Artificial Sequence
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                                                               Gaps
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APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth
APPLICANT: Franke, Kenneth
CURRENT FILLOWIN VIVEN 10/10/622,088
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: PCT/US03/2437
PRIOR APPLICATION NUMBER: PCSO/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR PRILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR FILING DATE: 2003-01-19
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 149
LENELLY SEQ ID NO 149
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0
Length 147;
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11.0%; Score 62; DB 21; L
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 62; Conservative 0; Mismatches 0;
Query Match
11.0%; Score 62; DB 21; L
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 62; Conservative 0; Mismatches 0;
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GENERAL INVOCATION:

GENERAL INVOCATION:

APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10013629.7
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 540
SEQ ID NO 223
LENGTH: 9289
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                                                                                                                                Sequence 199, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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  76 CTACAAATCGTAG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 10.1%; Score 57; DB 9; Length 92; 1 Similarity 77.5%; Pred. No. 4e-08; 69; Conservative 0; Mismatches 20; Indels
                                      Sequence 16, Application US/0989688BA
Fatent No. US20020116723A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION:
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,88BA
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US/09/946
FRIOR APPLICATION NUMBER: 60/049,946
FRIOR APPLICATION NUMBER: 60/049,946
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 16
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
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PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
NUMBER: OF SEQ ID NOS: 50
SEQ ID NO 15
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 69; Conserva
                           US-09-896-888A-16
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT APPLICATION NUMBER: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 199
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172 CTACGTTTCGTAG 184
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Search completed: October 25, 2005, 06:12:55 Job time : 1158.48 secs
                                 SEQ ID NO 1528
LENGTH: 986
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TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 345
LENGTH: 6289
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                                                                                                                                                                                                                                           7896 ААТТТАТТТАТАТАБССАААТААДАТТАТТАТАДАДТССИСТАССАДАДТТСАТТСАДАДА 7837
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| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: KUNST, Frederik
| APPLICANT: GLASER, Philippe
| TITLE OP INVENTION: Listeria innocua, genome and applications
| FILE REFERENCE: 344 702 - US
| CURRENT FILING DATE: 20303-03-27
| PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR FILING DATE: 2001-10-04
| NUMBER OF SEQ ID NOS: 4025
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-714A-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-345
                                                                             Score 39.6; DB 19; Length 9289;
Pred. No. 0.22;
0; Mismatches 74; Indels 0;
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Pred. No. 0.61;
0; Mismatches 75; Indels
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; Sequence 345, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
                                                                                Query Match
Best Local Similarity 53.2%;
Matches 84; Conservative (
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ORGANISM: Artificial Sequence
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Best Local Similarity 52.5%;
Matches 83; Conservative
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155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTG 214
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NAME/KEY: misc-feature

LOCATION: (1)..(end)

OTHER INFORMATION: n can be any nucleotide a,g,c or t/u
US-10-398-221-1528
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                                                                             TYPE: DNA ORGANISM: Listeria monocytogenes-4B
SOFTWARE: PatentIn version 3.0
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PAT 27-AUG-2002
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                  CQ610736 Sequence
CQ597683 Sequence
AE012382 Xanthomon
AC019883 Drosophil
Z92544 Human DNA s
AC133915 Homo sapi
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JP 200151625-A/1.

unidentified
SM unidentified
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E (bases 1 to 564)
S Grigliatti,T.A.A., Pfeilmann,D.A., Pfeifer,T.A. and Hegedus,D.D.
Insect expression vectors
Insect expression vectors
THE UNIVERSITY OF BRITISH COLUMBIA
OS Multicapsid nucleopolyhedrovirus
PN JP 2001516225-A/1
PN JP 2001516225-A/1
PD 25-SEP-2001
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AC088576 H
AF429315 H
AC099564 H
AC142495 H
AC142496 H
AC142497 H
AC14298 A
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AE003581
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PN JP 2001516225-A/1
PN JP 201516225-A/1
PP 26-MAR-1998 JP 1998541010
PF 26-MAR-1997 US 60/049946,28-JAN-1998 CA
THOMAS A GRIGLIATI, DAVE A THEILMANN, THOWAS
A PFEIFER, DMAYNE D
PI HEGEDUS
PC CI2NIS/08,CI2NIS/09,CI2NIS/09/CI2N9/22
CC Insect expression vectors
FT Source Location/Qualifiers
FT Source / Organism='Multicapsid nucleop
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AF429315_
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BD070856
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Best Local Similarity
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                                              RESULT 1
BD070856
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
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AX766573 Sequence
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AL939130 Erreptomy
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AE016781 Pseudomon
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(c) 1993 - 2005 Compugen Ltd.
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177
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Klysner,S., Nielsen,F.S., Bratt,T., Voldborg,B. and Mouritsen,S. Novel immunogenic mimetics of multimer proteins Patent: WO 03042244-A 60 22-MAY-2003, Patent: WO 03042244-A 60 22-MAY-2003, Pharmexa A/S (DK); Klysner, Steen (DK); Nielsen, Finn Stausholm (DK); Bratt, Tomas (DK); Voldborg, Bjorn (DK); Mouritsen, Soren (DK)
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Orgyia pseudotsugata nuclear polyhedrosis virus transcriptional
trans-activator (IE-2) gene, complete cds; ORF, complete cds.
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                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
Mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="p2ZOp2F expression vector for insect cells"
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/note="HindIII site"
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2128. .2133
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/note="AvaI, SmaI,
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/note="EcoRI site"
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/note="BamHI site"
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/note="ApaLI site"
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/note="Clal site"
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| db_xref="G1:404519"
| translation="WNWRWRYRRAKQQQVRVARQHRAAKLGRLYKAKKLRAELCEKLQ
LQRVNNDAALAKAFEEEFVYPHFSFYLYTLN"
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                                             411 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 470
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Wh.X., Stewart, S. and Theilmann, D.A.
Characterization of an early gene coding for a highly basic 8.9K
protein from the Orgyia pseudotsugata multicapsid nuclear
polyhedrosis virus
J. Gen. Virol. 74 (Pt 8), 1591-1598 (1993)
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/db_xref="taxon:164623"
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KEYWORDS
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NYNSNFVTSTECNHAVCFKCYVSIVCKESYKCSICNRTTISCRAYNRDGYVETTDI
NYNSNFVTSTECNHAVCFKCYVSIVCKESYKCSICNRTTISCRAYNRDGYVETTTT
NYNSDAJIKRHWAQLSDSNMPHSNEWTTIQELQAELARIRATTARAHIDVNWARSDSQ
LLRQQLDVKEAELAHESNARLKLQKQNETLSANNLSLQHQLNTQVIESRVKWEQFKRQ
HDEFMEKFKLSLS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2984. .3907

gene="IE-2"

note="ORF; homologous to the ACMNPV PE-38 gene; putative"

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/protein id="AAA46750.1"

/db_xref="GI:332542"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYCVQSNN I I DFLMPSECTHLFCYKCVLNMYKNÄMNVPRAAVSCPMCNKKVGTWQAFF
PNSVVSCKFT KKTGDRTPACLQFMLALKTIQDRYMATEEEARTEPSFVI KNLQAQLDA
AQKEARDLQESMERQKQAHNVÄNNSSCEQVTALQTTLADMQAQLDRSFALSSTLAEHN
RAANVQI DSLERRA VQEKLEAAQSAPVSVNVERNDNARQNTNLHERFRS YVYSTVSDWMI
EDSI KSLQSHVFGAACLPCSVNVEINPPPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /crānslation="msrsnnanaPtPsnrrrnlsLvrgrrltysPpDaasaQrasPPR
SAPRAAPRRVHAVGDPGAPLRASYALPNGVYNLHGDAHFNPPEEDDDILFVDTAAEQA
RQRAVNLHEAVNRHERLRRELGERMTRSPTLLNYSPSYSPTSRSRSPDLIMPEDLQP
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                                                                                                                      2 (bases 1 to 4170)
Thellmann, D.A. and Stewart, S.
Tandemly repeated sequence at the 3' end of the IE-2 gene of the baculovirus Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus is an enhancer element
Virology 187 (1), 97-106 (1992)
                                                                                                                                                                                                                                                                 nuclear polyhedrosis
1 (bases 1 to 4170)
Thellmann, D.A. and Stewart, S.
Molecular analysis of the trans-activating IE-2 gene of Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus Virology 187 (1), 84-96 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                             /organism="Orgyia pseudotsugata single capsid
nuclopolyhedrovirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="transcriptional trans-activator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                            Original source text: Orgyia pseudotsugata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 177; DB 14;
100.0%; Pred. No. 5.8e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="AAA46749.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="IE-2"
2984. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                        627. .634
/gene="IE-2"
657. .>1908
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/gene="IE-2"
2017. .2759
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2915. .2922
/gene="IE-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         557. .>1908
/gene="IE-2"
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Best Local Similarity 100.
Matches 1,77; Conservative
                                                                                                                                                                                                                                                                                virus DNA.
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/db_xref="taxon:164623"
/db_xref="inilar to Autographa californica nuclear
polyhedrosis virus (AcMNEV) deposited in GenBank Accession
Number 122858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALDNALVYNI VROLCDALNDLHNATGY IHNDVKLENVLYFGARDRVYLCDYGLCKRE
HSPVHDGTLEYFSPEKI RRHNYARSFDWYAVGVLAYKLLTGCRHPFERSADEVLDLAS
MRRRQQYNDPAALKNVRNLMARDFVFCLTRFNFECRSTDYKQ IAKHSFLASRHDYI"
                                                                                                                                                                                                                                                                                                                                  Orgyja pseudotsugata multicapsid nucleopolyhedrovirus, complete genome.
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RKTIAAHSFSADEINVHDLMSDHPSFVDMYFCYSSPTAWAIVMDYVPCPDLFETLQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ahrens, C.H., Russell, R.L., Funk, C.J., Evans, J.T., Harwood, S.H. and Rohrmann, G.F.
The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome
Virology 229 (2), 381-399 (1997)
                                                                                                                                                     CGAGGCCCCGTCCCCCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 656
                                                                                                                       CGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
TATCGGAACAGGACGCGCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA
                          Direct Submission
Submitted (06-MAR-1998) Oregon State University, Agricultural
Chemistry, Corvallis, OR 97331-7301, USA
Sequence update by submitter
4 (bases 1 to 131995)
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Submitted (26-OCT-2000) Oregon State University, Agricultural
Submitted (26-OCT-2000) Sy331-7301, USA
Sequence update by submitter
On Oct 26, 2000 this sequence version replaced gi:2934903.
Location/Qualifiers
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Submitted (23-0CT-1996) Oregon State University, Agricultural
Chemistry, Corvallis, OR 97331-7301, USA
(bases 1 to 131995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orgyja pseudotsugata multicapsid nucleopolyhedrovirus
Orgyja pseudotsugata multicapsid nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;

    .131995
/organism="Orgyia pseudotsugata multicapsid
nucleopolyhedrovirus"

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1 (bases 1 to 131995)
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GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT

CDS

CDS

CDS

CDS

CDS

CDS

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DVTKHPHLAVFMGRVEDRGVTQIAFARGQEBHFRKRKLEFEEGMDVDVRGRAPPLLA
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ASCVRRDIATARCLNSGHLCFDVARQLLDVSEVAARLSAWFRCGDATGLCADMORALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIDRHAPLARRVGRRANIFALDAIAĎIPSDVTNNLOGIIGREMHFPRCSGLARVADVF
DYDIRADGWWYHRCYULTYMHLVACOGNPGASATRIBOAVAHTIGRDBGGRAPAIAA
VYGRFCAIGREHFAHTTACMILLPOPMRNDLTPADBRHPCTGVIRDFGROCKDTYTD
LRTHADALYIHGTTDROKNALFDLCCVNASDIDADCYDCVNNKFYATQNKKYKM"
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APGYGLAENFERRRAVARHPLHYPTFGAAALTRRGGALSEWRLLNBFELLARRSDELL
KQOFGKSTPTIRQLRDNVQLLLLNLHPVYDNNRPVPPSVQYLGGGLHLAQALPQRLDA
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VALPRINVLAQKWFSQTAVLRHKNIVVAFVTQAGLQSSDEALQARVPMVCLPMMGDQFHH
ARKLQQFGVARALDTAAVSAPQLQLAIREVIADGEAYRARIDKLRAVVEHDAAPDEKA
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PIRHALGLPVGDHIHVYCEAAPTCAALPNAMPALYDYMVRRIGEGKRVLVHCYAGASR
SAALAVYYLMRSRQMPYQDALNAVQSKRRVAINDHFVRFLATRCSYRFVNDELKPQIV
                                                                                                                                                                                                                                                                                                                                    FPDRWHEYTACGAVIEGTRLLCFKVPLNAELFEYVTSDEDRWTAASVLARHSALGAVI
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protein id="AACS9013.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHCIKEEFANGGHKIRRLPKKVIEVDCAVNVAKDIVKKAILNKT"
complement (9094. 9825)
totce="ORP13; lef-1; similar to AcMNPV ORF14"
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                                                                                                                           to AcMNPV ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF14; egt; similar to AcMNPV ORF15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6819. .7814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11547. .12140
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100.0%; Pred. No. 5.2e-41;
iive 0; Mismatches 0;
                                                                                                                              /note="ORF10; ptp-1; similar
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                                                                                                  .6791)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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Best Local Similarity 100.0
Matches 177; Conservative
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                                                                                                                                                          TSLPRPOTSLPROTOASLPOOTPFDOPEMVSPPSFVHTTPALLPOTTOPPATDTFSRP
SDEFVYVPGKERAVPDTRFKPPVPPKPEHLKSRPSSVATNAAGATPVAPPPPFPSAD
VTTSMPPPPPFPSADVTTSMPPPPPMVDLATSMPPPPPPPPPPPPMVDLATSMPPPINNA
                                                                                                                                                                                                                                                             INNILIDAMVAETNKNAGDRRSALLDOIKOGKTLKKTOPADGAPATDPRSTILSBIRO
GKTLKKLRKIEDQSSTQTLLKDVDTTDKTKTILKNFVTNIDRISKQEQEEKDRLDTIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEDS FPIVNDQEVMDVFLVVNMRPTRPNRCYKFLAQHALRWDCDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVYIGTDSSEEE
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IARYLLAECGAVLVIDHPLDVFGETEEGVNELLEVQRINAGGDL"
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/note="ORF6; lef-2; similar to ACMNPV ORF6"
                                                                                                                                                                                                                                                                                                                                                     complement (2533. .3270)
/note="ORF3; ph; similar to AcMNPV ORF8"
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/note="ORF8; similar to AcMNPV ORF4"
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/note="ORF7; similar to ACMNPV ORF5"
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/note="ORF9; ptp-2"
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fumiferana multicapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta 2010gy 271 (1), 109-121 (2000)
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complement (838. .1449)
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VTHLLIKAENTYKPSNCAKWKĄVTKLCPKANMCKGLNPICNY"
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                                                                                                                       8 (bases 1 to 129609)
Carstens, E.B., Liu, J.J. and Dominy, C.
Carstensier, E.B., Liu, J.J. and molecular characterization of the baculovirus CfMNPV early genes: i.e.1, i.e.2 and pe38
Virus Res. 83 (1-2), 13-30 (2002)
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de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
                                                                                                                                                                                                                                                                                        9 (bases 1 to 129609)
de Jongy.J.G., Dominy.C.N.; Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
Complete Genome of Choristoneura fumiferana Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Microbiology, University o
Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B. and Krell,P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2002) Department of Microbiology, University og Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence update by submitter
On May 13, 2004 this sequence version replaced gi:30269978.
Location/Qualifiers
1. .129609
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/note="ORF3; lef2; Ac6/Op6"
/codon_start=1
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Submitted (13-MAY-2004) Department
Guelph, Chemistry and Microbiology
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/country="Ireland"
complement (1. .735)
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4 (bases 1 to 129609)

Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
Viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA replication
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                                                                                                                                                                                            128642 CGAGGCCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 128698
                                                                                                                                                                                                                                                                                                                                                           Choristoneura fumiferana MNPV polyhedrin, complete genome.
KFS12011 AET171329 S78506 S81690 U10441 U18677 U26676 U26734 U53854
U57401 U59008 U70432 U72240 X65395 S46001
AF512031.2 GI:47157118
                                                                        TATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu, J.J. and Carstens, E.B.
Identification, molecular cloning, and transcription analysis of
the Choristoneura fumiferana nuclear polyhedrosis virus
spindle-like protein gene
Virology 223 (2), 396-400 (1996)
                                                                                                                                                                 121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xie,W.D., Arif,B., Dobos,P. and Krell,P.J.
Identification and analysis of a putative origin of DNA r.
in the Choristoneura fumiferana multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee, H.Y., Arif.B., Dobos, P. and Krell, P. Identification of bent DNA and ARS fragments in the Choristoneura fumiferana nuclear polyhedrosis virus Virus Res. 24 (3), 249-264 (1992)
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Virology 209 (2), 409-419 (1995)
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6 (bases 1 to 129609)
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/locus tag="PP1884"
/note="identified by Glimmer2; putative"
CITATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAA 176
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78. .1985
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/locus_tag="PP1884"
2024. .4489
                                                                                                                                                                                                                                                                               Pseudomonas putida KT2440
Pseudomonas putida KT2440
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                                                                                                                                                                                                                                                                                                                                                                                                                      /product="baculovirus repeated ORF"
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VDRVYTNFHSHKURWYVGQLYSFPALSNFSLANQIYTGAPIFEKERWYSVITARHEDYK
NKLVIYPVTGISARGLVSGQINFDLQILTQKLLEGSSVYGKNQLPYKALKDYAISTNR
NKNLFKGLPRNVAVFYNERDITIALVEGEFEIDRIRLSGPLILRNIKQQ"
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/note="ORF9; ptp1; Ac1/Op10"

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/protein_id="AAP29803.1"

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VDEFQDRCFTMLVGVHCTHGLNRSGYLVCRYWVDKLGVSPADAIIRFEEARGHKIERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MYDANOIDKY1FVGGYYGDDKAMLQFIKKYDIASVISLINADVG
PIRQALGLPAGEHIHVYCEDAPTCVALPNAMFALYEYMTRRIGEGKRVLIHCYAGESR
SAALVVYYMRSRQMSYEEALSLVKNKRRVAISNHFVRFLASKCSYKFVNNVLKIRVS
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LCANVQLALAEI DKYAPLEKRYSIGNNI FALDTIADI PSNALDDFQTI I YEGFKDFVD
MNILAHVADVP DEPDRIKAREGWYYKFCVLTYWHRILVNAV PPTELMTEDADA UKFVQ
PONKGNCAPAMANVYGFFCGI GRKHFSQHKAASWYI LFQYMRNNLTPRDERHPSFGVI
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CNRFLDGVDKAPAVIIKPAAAGQHSSLICDKV"
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/trānslation="MHSVRNLFDSNMSLSSKLLVYAYYGAFNLLHEKYGESYHLYRIV
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/protein_id="AAR29802.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (2896. .3699)
/note="ORF7; Ac136/Op132"
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/note="ORF8; ptp2; Op9"
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complement (5854. .6387)
                                                                                                                                      2137. .2568
/note="ORF5; Ac4/Op8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHTVLINNNYAQDAPQFAI"
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/note="ORF6;Ac2"
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Best Local Similarity
Matches 37; Conserv
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Pseudomonas purga Ariz440

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonae.

Teachon, R., Pseulos, I., Weinel, C., Dodson, R., Hilbert, H., Fouts, D., Gill, S., Pop, M., Martins Dos Santos, V., Holmes, M., Brinkac, L., Melson, K., Daugherty, S., Kolonary, J., Maduph. R., Malor, R., Kosack, D., Moestl, D., Welson, M., Lee, R., Kosack, D., Moestl, D., Welson, W., Milte, O., Peterson, J., Khouri, H., Hance, I., Lee, P., Holtzapple, E., Scanlan, D., Tran, K., Moazzez, A., Utterback, T., Duesterhoft, A., Tummler, B. and Fraser, C. (Eisen, J., Timmis, K., Duesterhoft, A., Tummler, B. and Fraser, C., Eisen, J., Timmis, K., Duesterhoft, A., Tummler, B. and Fraser, C. (Eisen, J., Timmis, K., Duesterhoft, A., Tummler, B. and Fraser, C. (Eisen, J., Timmis, K., Environ. Microbiol. 4 (12), 799-808 (2002)

E. (bases I to 300363)

E. (bases I to 3003
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Pseudomonas putida KT2440 section 8 of 21 of the complete genome.
AE016781 AE015451
AE016781.1 GI:26557025
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SLRVDASSVDSKRLTFHLEREWLQSEVNRGKRFAFSYEFSRQGAQRRSQVLDLVLQRK
LYLPLPIIPDATQEDGDASYQGVVHPSRLESGAKVRIPAEAELGDGAEPAPTVNLHWE
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VSDFDQRSYPIIQVEGAENRELKLHEVPVGGALCTLPFWTFMAEGQLLGIEALGRSAS
GQDVTHILRPPTEAVTYDBYSDGVIKAYLPRQFLGNLDLGKDFRLTVSASFDDGETWR
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124634 CTTATCGCGCCTATAAATACAGGCCGCACCGAACTGGTAA 124595
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/strain="KT2440"
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CRAYIDLITDELSLKDVLKRRYSGDRVSMELVTVHTATADFTRYEETVATPOSWTWGH
ACCGLWHAETINVETTASWQIQDLQGATIKIEEVKHKIYRYQGGSFKFEGDPYEDQISA
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APMESDDAADVDGALVGLVAMGPSNGPQNMPGPESTRYLIPDDNGDYSATVLLDKAWVA
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MDKTDGLLSLSVHDLLDPLPVTQTVPLSADAQGVSADLREGTDTELDLGGGLPQRQAA
GRFFKEVLSGLGSARQVYPLADFKALSGNPYLAVRHSEVRTHVSKADGKSALVIFAGI
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QPLLSVTFEHDEVRQHWKSHCTLTFTYKPKPTGPLYSRTATFQFDLQTVFTLNAPASP
EESAGCMLLGQVLWPWQAAEVTEVSGLPSDTPSDLREEIYAFVAFLVKQAVLEGLARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTSKQAISMASVAPATLIVNPLIRVCYFDDTLTLTAGAOTGDLDMSVVDDGEEGRGSV
VAEGOGRRCYTYAGSKUDAWAYVLDQVRVQNRETSESRSIYVLVRQRRPELVIDVKQ
LPDGDLOLTGMFDGVQOPDTOWALPIAGTGEIDEATGRYSPAASADADARFALITAKWA
IPGSVÇITLEGHLILPLDLSLHFDAARRAASPTGLRVATSPSIGG"
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/dx xref="G1:24983394"
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/translation="WMPHHPLEVETWSVSLEALEFGTPLLSFSNASTSDAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTMNÍIKGTVNNSGKLVSSVEINEASGYWLOMEVDLETVRGEVHPYGLVALNLAKGG
TRISNLEEDRENDLAQQULDALOAMMSENGRGKARE ELGYVPRAGYEDTYPTGRILKTQ
RAPGARVRDANYYGGAVLUFIRLRDSILDGQPPGTGYPYLLPDGDVSATLVLNKDML
GHASDDGLELLARLLFPELNAFVKKVDSTPLDRVMFGNIDPLRTQLTVKFPTMGTVVTA
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CEVVRNGVVFAAGYSVVKETAVKAISGWVDLQRFALTVGKSPDGVIGTVGSNGYQQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYSNDTRHQNAEIEVKVHTPDAYKSTDYTFTRTRAAGGGGNSGSTDFEHEDFDLHPET
DDWMLSYNHOTFYTAEPKYKAKSDNDRDWTSWYRWRBSFPGBYYKSYTGYYPQYN
EPLPKFVSFDPDSKELLDGVEREVSSYYQPGLLAIVWYRRRDLFPRTSDHRALFEKL
SKPLRVQLRDAHANLHIIQIDYLPADTIGDRNILAHTVPSRPTGRQTSITRLSNYQBG
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IIKAEYKQGEETYHAAARALVISEPVLAMPAFGAYRPQESANGIDLMNAGKGNVSFEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFIRANESLMATEGOGPOPAAPRGAEDRTIRLOMFLHRRGASTSEVFYAGFOARTGRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNGSVGNLPAEQSDYPFLLPDDLAQPVDSALLLTSRFLHRAAYATGLAQMLEGGAFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTAMI PEQVMAGLSLADGKRLVPFDFQLPDGMAVFASGYGTAGMRI VDRPVTLAPGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTFSVEPPREGLTWSLEALPGTVGDLGRIDPASGEYRAPPAHAMAGKPVRVRIIATDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1549. ~6903
/locus tag="PP1885"
/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by Glimmer2; putative"
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note="identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549. .6903
locus_tag="PP1885"
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transl_table=
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10329. .14201

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160996 TATCAAAACCTGCAACGCCTGCACCGCAAGCTCGCAGCCTATCTGGAGCAAGCCCGCGC 160937
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QCDASADVBANPVDLGEWSYNDFTCBGFTTPPAAFQVRLSNCQVDPDPGNETLATIEL
DGINGSRPIGPADENVFSLTEDBSAARGIGIQMLYNGVSMPLNKEIDLVPLTSDNVPLN
FQARFQTEPNSSLETGLAKGALNFTRYR"
COMPLEMENT (15402. .17897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                 /translation="MMSTSTSVHSNAFNFSSYIESGVDPRTGQYTVSIRLPELQGNDL
QGPGFELALFYSPLNGEDSGFGKGWNLQLTQVRKHIVTLSSGETYKITGKSSVTGRLE
MKEQKLRQFDLYEDPPGPGGAARFRVEHRSGLVEVLEVMGSGEGEVALPVELHSPLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSESDNRVSEĪILPTANQARMRFTYEDVLĞYLCVRECTTPYGGVERVFYQDAGHKFPS
SAARDKNLPRVTRHEIDPRFGQAAKVVRYEYPGTHNPIGGGSSISWSDDGLDNLYKVP
EDYTYKSIQIQEVRRQSVRTITRTFNRFHLLTEQATAQGDKLLQAFTRYADNAGNFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEPYFOLPHDETQRWSLISNPSRQRBEKRVTRYDSHGNVLTRLLPNQVLETNVWYSAE
EGDBHGFYRNLKTRYQPAATGHGAATLTQDGYDYALPLGSYLKQPWRLLBSETL
SEGSSAPGTFLEKISKLYQBESABRFSYGRYQQTVSYPGVDGSPFDTLTHYGYSLD
DDERALQTVEKLVGVDGESKTITLRHALDTGEPLLNLDDNGVEIRYYYDALRRVTREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAPCKPFEAERNYKYFLCAYDNEQAQQWAYDVKQVETHTLLDGLSRPIFEERADKDSA
TYACALRPIYRARYDELDQLVEETEIDWLGDCLLELTSHISYDDWGQRYAVLNPDGTT
QVEEIDQVASTDGPVHRAWREVEHSRVSGITETWYNLFEKFVRIERFALDGSTSISLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNDYDGIGRLSREAGGSGAGGRUVEYRYDAFDRVREERLADRVNTVYRTYAGHSRNDL
VROYSKKOWITSEAAVLLGGOVPDGLERRYVAITGGREGPTERDYDDERROPTER
IEYOYRPALGEEPVLKALGSCREAKEYDLKARLTHGEEPGDDENSGYTLDRSHFLSN
GEVKRESRTVDGEAFSMTYDYSFRSRLRAYVDVLGGTQLYDFDDVGRLEKTTLHAPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRTRYRLORAPAROLLLLESTFGYDROGRMASITTTTÄSTGHALATLLEYDEFDREIL
RTFDFGDTVQTLAQDYDEFDCLKSRILKERPKGSDESQATLLRHETYQYDRRGRLQIY
TCDGPEAPVDPSGQTIARQIFGFDGLDNILSVITYRPDGSWQRTLYEFKNSDPAQMSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAN67567.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIPPDALLETYDVÖHDLEËLFKIVKYDPQLAIDLHYDGNGNLISDEQGRVLTYDGLNR
LLRVETPDGERCRYNYDPENILSGTAPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHVRDLNTLYVPRDARIGTTIGTFELFEATLOQNNLALLCRTYGERINFNFQAARGVH
PPLPAVDGRFLDAPVLRTNIPGIGAIVELLHPFLGGTDQFIPDSRPPRVPFTAYYEQT
                                                                                                                                                                                                                                                                                                                                                                                                                   RLHLSYLPFGQGHMRLSEVQDESDVLLRLQRSDNSRVELLCYPSGGDDGGPLARYAMT
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                          10329. 7.14201
/locus_tag="PP1887"
/note="identified by match to TIGR protein family HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus tag="ppp1888"
complement(14251..15345)
/locus eag="pp1888"
/note="similar to SP:P42185; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 300363;
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                                                                                                                                                                                                                   product="hypothetical protein"
protein id="AAN67506.1"
db_xref="G1:24983396"
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
/product="fimbrial_protein"
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54.8%; Pred. No. 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (14251. .15345)
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locus_tag="PP1887"
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/transl_table=11
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                                                                                                                                                          codon start=1
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                                                                                                                               TIGR01643
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Best Local Similarity
Matches 69; Conserv
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SOURCE

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coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                             The RPCI-24 BAC Library has been constructed by Pieter de Jong and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Likely pseudogene (HMM Sc=39.91 / Sec struct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Likely pseudogene (HMM Sc=33.79 / Sec struct
                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                      1. 155274
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                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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/chromosome="9"
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8388_ .8550
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1. 165
/rpt_family="B2"
/rpt_family="B2"
/rpt_family="Alu"
288 . 309
/rpt_family="Alu"
288 . 309
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5566_ 5711
/rpt_family="Alu"
5712_ 5786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="B4"
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1130-_.1302
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1855. .49p^
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/5788. .5975
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5316. .5565
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1876. .4987
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7670. .7741
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1010. .1081
http://genome.wustl.edu
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                                        SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                            /map="9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9947.
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                                                                                                                                                           AC121979 155274 bp DNA linear ROD 13-NOV-2003
Mus musculus BAC clone RP24-289L14 from chromosome 9, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing of Mus musculus
Unpublished (2001)
3 (bases 1 to 155274)
Direct Submission
Direct Submission
Submitted (21.MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
(bases 1 to 155274)
MCPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-4042 2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 155274) MCPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this forde. It may be shorter because we only sequence overlapping clone sections once, or longer accouse we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-NOV-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 6 (besses 1 to 155274) Wilson, R.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (195274)
McLellan,M., Cotton,M., Doebber,A. and Schatzkamer,K. The sequence of Mus musculus BAC clone RP24-289L14
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Nov 2, 2002 this sequence version replaced gi:22476161.
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Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BB0289L14
                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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45478 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCACGG 45537
                                                                                                                                    CR361569 17-0CT-2004 Danio rerio clone CH211-99120, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-077-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@senger.ac.uk
On Oct 11, 2004 this sequence version replaced gi:51592229.
                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry Determinator; 100% of reads
Consensus quality: 175712 bases at least Q40
Consensus quality: 17532 bases at least Q30
Consensus quality: 176923 bases at least Q30
Insert size: 178471; sum-of-contigs
Insert size: 179905; 5.5% error; agarose-fp
Quality coverage: 7.91x in Q20 bases; sum-of-contigs Quality
coverage: 8.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as true of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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CR361569.5 GI:S4035037
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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Contact: zfish-help@sanger.ac.uk
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                                              /note="Likely pseudogene (HMM Sc=33.19 / Sec struct
Sc=-10.52)"
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51.7%; Pred. No. 48;
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/rpt_family="RMER6B"
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1574_..16035
/rpt_family="RMER6B"
16036_..16182
/rpt_family="Alu"
16183_..16352
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16502. 16576
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17406. 17489
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1625, .11800
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2916. .13104
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7672. .17818
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7585. .1791
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rpt_family="B2"
1348. .11466
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1472. .11624
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rpt_family="B2"
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2291. .12465
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3112. .13274
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rpt_family="L2"
8767. .18948
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.8962. .19079
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1349. .11370
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (07-MxR-2011) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Taukuba, Tbaraki 305-8602, Japan

(E-mail: teasakianias affrc.or, Jp WRL: http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jul 17, 2002 this sequence version replaced gi:20975425.

Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr. (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RRP. Protein homology of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DBUJ accession no. and RGP clone 1D.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein'. A gene without significant homology to any protein but with a gene prediction program is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from Misrev to -21M13 of the BAC clone. This sequence of OSUNBaOO14KOB clone has an overlap with PO443E07 clone (DDBJ: AP003768) at the position 1 to 45,852 of 5 end and an overlap with PO441E12 clone (DDBJ: AP003768) at the position 1 to 45,852 of 5 end and an assembly quality together with annotation of this entry is available at http://rgg dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(1396..1701,1758..2043,2410..2544,
3405..3547,5088..5199,6055..6167,6605..6690,7352..7491))
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                                                                                                                                                                                                                                                                                 Sasaki,T., Matsumoto,T., Yamamoto,K., Sakata,K., Baba,T.,
Katayose,Y., Wu,J., Niimura,Y., Cheng,Z., Nagamura,Y.,
Katayose,Y., Wu,J., Niimura,Y., Cheng,Z., Nagamura,Y.,
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Yano,M., Jiang,J. and Gojobori,T.
The genome sequence and structure of rice chromosome 1
Dature 420 (6913), 312-316 (2002)
                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Direct Submission
              clone:OSJNBa0014K08.
                                           AP003376 BA000010
AP003376.3 GI:21902027
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                                                                                                                                                       ORGANISM
                                        ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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AUTHORS
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP003376 177263 bp DNA linear PLN 31-AUG-2004 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
154564: contig of 19806 bp in length
155 154664: gap of 100 bp
155 179571: contig of 24907 bp in length.
15cation/Qualifiers
1. .179571
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              134759
154565
154665
                                                                                                                                                                                                                                                                                          misc_feature
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LOCUS
DFFINITION
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                                                                                             FEATURES
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148416 GTGACAGCGGACGTACGTAGTGTTGGAATCTCGCCCGGTCGAATTCCTTGGCGCAA 148475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     31903. .31993,32132. .31242,31391. .31579,31787. .31815,31503. .31993,32132. .32306,32410. .32549,32638. .32770,331508. .33574,34086. .34243,34332. .34405,34496. .34609,35132. .35437)
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                                                                                                                                                                                                                                                                                                         AEALRSAAVAFGCEQVVGHGVDRSLVSAALRHVAAATARAATPEPEEVEVNGDDENGE
EMWWSFGGGGGBAAGNWALGSGASHRTADALFT OLDEGTATKIMDVLGRGGAVATQS
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TAAADTNGSLICI RRHRRQDDRSTRADDILMLVRSSRGSRALHLCPGA
SAFHI FSRRGWSRFRPMDGAVVVTVGDQLQACNGGLYKSVAGKPAYSNDDLRGNGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GVASAELFYCFPSAGTAAGKASEVLSADAGKIIPLNLQFMVAACLVLGYHFLLSSLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKWRDASTGLHVDYDORPDVFREFVEYVVNLKFDEEPNYAKCISLFDTVVGPNPDIRP
INTDGAQKLIHLVGQKRGRLLMEETDEQPKKKIRMGMPATQWISVYNARRPMKQRYHY
NVADSRLVQHIDKGNEDGLFISCITSCSNLWALIMDAGTGFTSQVYELSPHFLHKEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDOWERNYY TALAGANNGSSLVVMSKGTMYTOOSYKVVELDFLYPSECHORWDNGY
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join (39834...39907,40580...40722,41299...41408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MPYVVGTTGSNCSEAIVIRSSLISRQKEEYPKGYGKSELANPPM
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SIFPPC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join[31081 .31242,31391 .31579,31787 .31815,31993 .31993,32132 .32306,32410 .32549,32638 .32770,35308 .32574,34086 .34243,34332 .34405,34496 .34609,35132 .35437)
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/gene="OSJNBa0014K08.7"
   .29650)
                                                                .29650)
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   .28537,28795. .29152,29378.
                                                             .29152,29378.
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                                                                                                                              'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
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53.1%; Pred. No. 71;
iive 0; Mismatches
                                                             join(27978. .28537,28795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oteIn id="BAC05583.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="OSJNBa0014K08.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon start=1
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148536 CCGGCCCTCT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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21203 . 221300,22377 . 22481,22872 . 21649,21807 . 21899,
21991 . 22020,22277 . 22431,22872 . 22967,23073 . 23252,
24422 . 24585,24909 . 25092,25170 . 25493)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join[19222. .19261] 19694. .19848,19915. .20022,20628. .20832, 21203. .21300,21397. .21480,21572. .21649,21807. .21899, 21991. .22020,22277. .22421,22872. .22967,23073. .23252, 23347. .224585,24909. .23653,23956. .24011,24094. .24347, //gene="OSJUBBOO14K08.4"
   .6167,6605. .6690,7352. .7491))
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SMSST VECLIAALKDNVATQLGGHISNSTAKTPI RRKLELRETDGPVLSVATPGKTYP
SQORS PLLSGQKINEVVEKGTGTTDLPAAKIS EMLISNSLDNAPTGSLLRVVNGILD
ESIERKGEE PREVANTUGETERTRIGADHIRNONSI IKTREDKYRSKIKALE
TLVNGTNERNEMAINRLEVVKVEKSKI DEKRKLGEQDMIRLIREKERARNI I ASLHQE
MQCWNRWHEGPREDLKGLUDAAENYHKVLARNGKENRYGTHSKOAEKGNIRVCRVRFEPLPG
QDGKLTAI DVI GENGEIL JADRAENYHKVLARNGKFGHRSGABEVFSDIQPLIRE
VLDGFNVCI FAXGQTGSGKTYTMSGPGTSREDMGVNYRALNDLFDISLSRKNAFSYES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRAVGSTALNERSŠRSHSILTVHVRGLDVKNGSTSRGCLHLIDLAGSERVERSEATGD
RLKRAQHINKELSALGDVIFGLAQKNAHVPYRNSKLTQVLQSSLGGGAKTLMFVQINP
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                                                                                                                                                                                                                                                                                                         AAIAHLKRCGFYLEKLAKKGRGNSPQRRGGAPRRLRVPTGNEEDDPPPLAPFALPLGR
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FGLIPRMRSLRLRSGRRRGESGGDQAGALILSWVDANYRGYLDEGFCQVEDLQDEASP
NFVEEVVTLFFKDSGRLMSNIEQALCMRSFQKVKREHAVLRQKLESYFQLCSCTWAEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKGILADDRLAKKPSRQYSMEKGSATNRAIPDFRSAAAMSDAMRRARRRSPCHARNTR
NGTRRAGARPDPEFSRQPIRVLGGRSLSVDETWVTSPAAAVFLRHGETRAPAFALGTA
GRRRGEDDMSVIR"
                                                                                                                                                                                                                                                                                                                                                                                                                           join(8072. .8086,9178. .9387,9474. .9671,12990. .13120,
14072. .14144,14960. .15376)
Gene="OSJNBa0014K08.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oin(8072. .8086,9178. .9387,9474. .9671,12990. .13120,
4072. .14144,14960. .15376)
gene="OSJNBa0014K08.2"
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                                                                                                                                                                                                                                                                                                                                                                                                       RHHDRMPSRHLRPSRAAAGQIQAREGRIRPWGLRIRRLLPTLPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(16191. .16218,17138. .17280)
gene="GSNBa0014K08.3"
join(16191. .16218,1138. .17280)
gene="GSJNBa0014K08.3"
405. .3547,5098. .5199,6055.
gene="OSJNBa0014K08.1"
                                                          note="hypothetical protein"
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HTG 15-NOV-2002

linear

DNA

222256 bp

AC134482

RESULT 11 AC134482/c LOCUS

LMIVPVRLRTGT

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Marany, Danders, Marzher, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Albarbooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Avogaja, A., Ayodeji, M., Baca, E., Baden, H., Balabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Dayagia, A., Ayodeji, M., Baca, E., Baden, H., Baladranale, E., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blatt, C., Carter, M., Carter, M., Carter, C., Cavara, D., Chen, G., Chen, C., Coyle, M., Cree, A., D'Gouza, L., Cavara, C., Coyle, C., Coyle, M., Cree, A., D'Gouza, L., Davila, M., Cree, M., Divana, L., Davila, M., Cree, M., Divana, L., Dayala, C., Cockrell, R., Cox., Coyle, D., Danson, S., Daramo, C., Ding, Y., Dinh, H., Divana, C., Coyle, D., Danson, S., Daramo, C., Ding, Y., Dinh, H., Divana, C., Coyle, Danson, S., Daramo, C., Ding, Y., Dinh, H., Divana, C., Coyle, C., Ding, Y., Dinh, H., Divana, C., Coyle, C., Coyle, C., Ding, Y., Dinh, H., Divana, C., Coyle, C., Ding, Y., Dinh, J., Bivana, C., Bernandez, S., Pinh, M., Plagene, C., Pana, C., Pana, C., Handle, C., Hardle, M., Garrer, M., Marth, R., Martin, M., Morris, S., Marter, M., Morris, S., Marter, M., Morris, S., Marter, M., Morris, S., Marter, M., Ma
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-SEP-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston TX 77030, USA Baylor plaza, Lo 222256)

Rat Genome Sequencing Consortium.
Rattus norvegicus clone CH230-179K4, *** SEQUENCING IN PROGRESS
                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Genome Sequencing Consortium.
                                                                                                   GI:25007228
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Unpublished
                                                                                                                                                                                                      Rattus norvegicus
                                                                                                   AC134482.2
                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                    ACCESSION
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Baylor Plaza, Houston, TX 77030, USA on Nov 15, 2002 this sequence version replaced gi:23334632. The sequence in this assembly is a combination of BAC based reads and whole genome shotgour sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* NOTE: This is a "The true order of the pieces

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2737 AACTAGACCCCGCTCCTCATCAGCTCAGTACATTCTCTCTGGGCCTGGACCCCTTCTATC 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 ATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap, version 0.990329
Consensus quality: 190050 bases at least Q40
Consensus quality: 194119 bases at least Q30
Consensus quality: 195064 bases at least Q30
Consensus quality: 195064 bases at least Q30
Estimated insert size: 204504; sum-of-contigs estimation
Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 222256;
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107900 107999; gap of unknown length
108000 222256; contig of 114257 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.3%; Score 32.4; DE Best Local Similarity 53.1%; Pred. No. 71; Matches 69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (113301. .114059)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: CH230-179K4
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1. .222256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2617 AGAGTGCTGG 2608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON NOV 20, 2002 this sequence version replaced gi:24158508.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap, version 0.990329
Consensus quality: 206551 bases at least Q40
Consensus quality: 211776 bases at least Q30
Consensus quality: 215202 bases at least Q20
Estimated insert size: 208321; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.3%; Score 32.4; DB 2; Length 270958; 53.1%; Pred. No. 70; ive 0; Mismatches 61; Indels 0;
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555 248654: gap of unknown length
655 267829: contig of 19175 bp in length
830 267929: gap of unknown length
930 269946: contig of 1017 bp in length
947 269046: gap of unknown length
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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A. Crganism="Rattus norvegicus"
/mol_type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-6908"
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Center clone name: CH230-6908
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248655. .249752
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246116. .248554
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                                AC145655 20-NOV-2002 Rattus norvegicus clone CH230-6908, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
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                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                             HTG; HTGS PHASEL; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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TCHAYDSDGGRALAGAITSLMTCTSYKRSAELAAVOEPYDGYARNAQPHQRVWKQHSD
ANGVAVRVDDLDTPIWAATTEAWQDVLHLGERNGFRNAQASVIAPTCTIGLAMSCDTT
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PKQAHTGAELVENQLGTQADAPLCFSCGTKMQRAGSCYICEGGGSTSGCS"
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DITSVQYQNDANNSVRVNDTFWKAVBEGGKFGLTSRATGGEVIEBVDAKSLFRKMARAAW
ACADEJQYDAINSWHTCPPSGRINGSNPOSESYMHLDNTSCNLASINLWKFKDDGK
GRQSFEVERFAKVELELITAMDISICFADFPTQKIGERYRAFRQLGIGYANLGALLMA
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GFLRRDPHRPRAYEVRGSDQSSSVQPTDTAGKPAASYVPLVGRIAAGGPILAEESVED
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/gene="lexA"
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                                                                                                                                                                                                              105820 GTTAGCCAGAAGTGAGAACAGGCTCAGGTCCCCTTGTCACACTTCTAAGGGAAGGTCAC 105879
                                                                                     105760 AACTAGACCCCGCTCCTCATCAGCTCAGTACATTCTCTGGGCCTGGACCCCTTCTATC 105819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M. and Omura, S. Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT 10-MAY-2003
                          44 AGCCGGACGCAACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTC 103
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Submitted (29-MAR-2002) Director-General of Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center, 2-49-10 Nishibara, Shibuya-ku, Tokyo 151-0066, Japan
(B-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
TEL:81-3-3481-1933, Fax:81-3-3481-18424)
This work was done in collaboration with Harto Ikeda(*1), Jun
Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi
Shinose(*4), Hioshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi
Osonoe(*4), Norihiro Kakshida(*4), Hideshi Kikuchi(*4), Tadayoshi
Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7)
and Satoshi Omura(*1,*3)
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*2 National Institute of Infectious Diseases
*3 The Kitasaco Institute of Technology and Evaluation
*5 School of Science, Kitasaco University
*5 Chool of Science, Kitasaco University
*5 Institute of Medical Science, University of Tokyo
*7 RIKEN, Genomic Sciences Center
Pollowing url is also available.
http://avemitils.ls.kitasato-u.ac.jp.
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Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
Kushida,N., Director-General of Biotechnology Center, Shiba,T.,
Sakaki,Y., and Hattori,M.
                                                                                                                                                   104 ATGCGCGTGACCGGACACGAGGCGCCCGTTCATCGCGCCTATAAATACAGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avermitilis genomic DNA, complete genome, section 11/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
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Streptomyces avermitilis MA-4680
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AMLKGRSNYLCLHRLHEGVPQDEEBGLPDQFBAAPTSKLGQDLLRLRDWSDETETGD
DRDLTPGVSDRAMQVSVSSRECLGATKCAYGABCPABMSBRAKLABVVVTNHALLA
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AVRKQALASVESVHDVAERITNGSEMDVVWYERHDRFGASLRVAPMSVSGLLREKLFA
                                                                                                                                                                                                                         DRSVŮLTSATLKLGGDFNGVGASLGLAPEGTQGDDLPQWKGVDVGSPFDÝPKQGILYV
KHLSRPARDCDRADMLDELTELIQARGGRTLGFSRRAAGLAAEELRSR IPEPPIL
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ARQKAVEDAGGNGFWAVATHAALLMAQGAGRLVRASGDRGVVAVLDQRLATARYGSY
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ADLOSLARHYPARPHTGIHLLIGGYADRGRGLGSTLLRAVADLVLDRRPSCARVVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MPPTDASTDAEPATSADPARIAVSARSAADSEDTLELRLPDELV
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TQAPLAPATQVVFVPEVRTPVVQASESVPPVCRARESERLKGTTADPLDHPEAQTAA
QAAAVENLLRCWVRENGLVAPDDGTLRIPLLATGTALLVPVHHWSPTGWHRFGLPYLA
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AVFIDDRRARPADEPDLFLAAEQALLLGHPLHPTPKSREGLSBAEARLYSPELRGSFA
LHWLAVAPPVLATNSAWTERGRPVPAEQLTARLAGDGLPMPDGFAALPLHPWQIREIR
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RKELHRGVEVHRLLRSGLGEQWQAAHPGFDIVRDPAWLAVDDQHGNAVPGLDVMIRHN
PFAPTDDVSCVAGLVSPRPWPQPTEQPRPVMRSRLAEIIIRLAGRTGRPRGAVATEWP
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RFLADVATGPARLRTPLPTRLLDSPVLRCKANLLTRLHGLDELVGPVDTQSVYVTIAN
PLHS"
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YHGMTAGALEASGGATDGRVARLPYPQDYRCPFGIGGERGAELGARWTESLLDDVKSG
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ENSGVVPDVMVLSKAIGGSLPLAVVVRDDLDVWQPGAHAGTFRGNQLAMAAGTATLA
YVREHRLABRAQTLGARMLDQLRSLATEPPCVGEVRGRGLMIGVELVRABEDREAVSP
GSGDFASLDYTAGAGRPAAPELAAAVQRECLRRGLIVELGGRHASVVRLLPPLTISDE
QATAVLDRLADAVEAVARGRAERSRGFQRSERAG"
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DTRASSESSPSASSAGDDKIKIPDDIRDKLKERGIDIDKWKWGAWKWWNRDDWLRBAN
<u> DAGTGTGKSLGYLVPALAHGERVIVATATLALORQLVERDLPRTVDALHPLLRRRPEF</u>
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/protein id="BAC70178.1"
/db xref="GI:29606115"
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transl_table=11

/product="putative secreted protein"

/protein_id="BAC70179.1"

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/transl_table=11
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/note="SAV2465"
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'note="SAV2468"
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7

DB 1; Length 299550;

18.2%; Score 32.2; I 61.2%; Pred. No. 80;

Query Match Best Local Similarity

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128986 CCTCCACGAACCGGACGCGTCGCCCTTGATGATGAGGTTGAGTTCCTGCACCAGACCGG 129045
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PI JULIE SUDDUTH KLINGER, CHRISTOPH REINHARD, KLAUSE GIESE, FILIPPO PI RANDAZZO,

PI GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE PI BRANDAZZO,

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Williams, L. T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., and Crain, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V., Jones, L.W. and Crain, B.S.
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RANDAZZO,
GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE
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RADOMIR CRKVENJAKOV, MARK DICKSON, SNEZANA DRMANAC, IVAN LABAT,
DENA LESHKOMITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 gecercina a necescrite contractor de contracto de contracto de contracto de contracto de contractor de contract
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58 CCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGG
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Patent: JP 200254055-A 2465 15-OCT-2002;
CHIRON CORP, HYSEQ INC.
CHIRON CORP, HYSEQ INC.
CHIRON GAPIENS (human)
PN JP 2002534055-A/2465
PP 13-MAY-1999 JP 2000548466
PR 14-MAY-1999 US 60/085426,15-MAY-1998 US 60/105234 PR 15-MAY-1998 US 60/105837
PN 14-MAY-1998 US 60/085696,21-OCT-1998 US 60/105234 PR 15-MAY-1998 US 60/105837
PI LOUIS T WILLIAMS, JAIME ESCOBEDO, MICHAEL A INNIS, PABLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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/organism="Homo sapiens"
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1. .921
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                        118 ACACGAGGCGCCCGTCCCGCTTATC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BD221352.1 GI:33031122
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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BD221352/c
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VERSION
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AUTHORS
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JOURNAL
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complement (1247...1858)
/note="ORF 3; lef-2 Op6/Ac6"
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/product="late = wpression factor 2"
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                          PLNVMPPPPPPNVPPPPPLDNLLLDAMMSEPRKGATDRSALFDOIKWGATLKKAQPVE
PSDLKGGMINOIRTGATLKTGRLEBDBNLGKKRGREGILGVLYNTULGSRRGGIDSE
RSDVATSEGTSGPDSSADFRAKGSKSELKHAAHLYNFAKDSKLYNTQKVNNSELTKI
LENVGPLLKRSPRTAENVEKANAGLYLFRQHVTLPKNALDAQPAPELYAADAPQFYVQ
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TGFDCNRILLELSSSSNDVITKSPVIIKNSAATVGQSALVCDKV"
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NGVNLNTTLKPPVPPKPAHLSRPNFMFVGDKVTGNTPPPPNGTSPQPGVNVPPPPVAP
                                                                                                                                                                                                                      complement(1. .738)
/note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                                                                                                                                IEDLLFAGRYDDARAFIQAVDAPEDMKLKKFLTVANQLSTRGQ"
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(protein id="AAQ91731.1"
(db_xref="GI:37499332"
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/product=basculovirus repeated ORF"
/protein_id="AAQ91674.1"
/db_xref="GI:37499275"
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/codon_start=1
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/db_xref="GI:37499297"
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/note="ORF 6; bro Ac2"
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/note="ORF 2; Op5"
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/note="ORF 5; Op8/Ac4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ORF 4; Op7/Ac5"
                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="unknown"
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/product="unknown"
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VLASTVANTENLLKSDAVNDVSITVLSGDFYEEYSRYATRQYVSTDTLPPPPPLTPPI
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PVAPSPQATQTPSPRQTFAAPSPVPAESPQPTRAFPTPEGTLSRGAADEFEYPAGTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "I (bases 11500 to 13512)
Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UPP-glucosyltransferase gene from two distinct nuclear polyhedrosis
viruses isolated from Choristoneura fumiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The putative LEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases
                                                                                                                                                                                                                      AY327402 131158 bp DNA circular VRL 08-OCT-2003 Choristoneura fumiferana defective nucleopolyhedrovirus complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canada
On or before Oct 8, 2003 this sequence version replaced gi:1117788,
gi:2581770, gi:1754838, gi:4092491.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrett, J.W., Lauzon, H.A., Mercuri, P.S., Krell, P.J., Sohi, S.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                (CEDEFNPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry
Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M. Characterization of an overexpressed spindle protein during a baculovirus infection
Virology 268 (1), 56-67 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
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X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Choristoneura fumiferana defective nucleopolyhedrovirus Choristoneura fumiferana defective nucleopolyhedrovirus
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/organism="Choristoneura fumiferana defective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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join(12949. .131158.1. .20)
/note="ORF 149; 1629 capsid Op2/Ac9"
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Submitted
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EINCHAPLETRCASRVOAFFALDSLEFPRNMTDSLQVIMGRRWHFVRGYALTHVANVF
DPTIKLDGWWYNKFCVLTYMYRIIRGTVPABLITRLQNVVTKYIKPEYDESNNALAMG
DPTIKLDGWWYNKFCVLTYMYRIIRGTVPABLITRLQNVVTKYIKPEYDESNNALAMG
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6450. 6723
/note="4 copies of a 30 bp imperfect palindromic sequence;
location similar to Ac hrla"
complement (6723. 7871)
/note="0RF 10; Op20/Ac20"
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TRRYFHHVVPGARGNCASIVOGLDTTTASHFRYGCVNTYTTSGGCGGGBA
VTRYRHVVPGARGSYPLSGNGLDEPTHRFFLDTRSRIRYNDVRGLIN"
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PIRQALGLPAGYHIHVYCEDEPTCMALINAMDALYDYIERRINEGKKILIHCHAGVSR
SATLAVYYYMKKWQVSYEKALRFVNNKRNVALSDHFVRFLSSRCTYRFVNNKLKIHVG
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product="actin rearrangement inducing factor"
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/note="ORF 11; arif Op19/Ac21"
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; Pred. No. 94;
0; Mismatches
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/note="ORF 12; Op18/Ac19"
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BQ720271 BB340052 BB8434052 CG295117 CC190317 BX823015 CK192985 CC00683015 CC0683016 CC0867977 CC886875 CC88687710 CC8867710 CC88677710 BU140827 CC875979 CC245979 CC245979

603137854 CH261-136 BY342724

Pan trod]

FGAS00139 Mdfrt3029

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AQ297217 507 bp DNA linear GSS 15-DEC-1998 HS_2266_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=15 Row=A, genomic survey
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1 (bases 1 to 507)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Hood, L., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Concact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="Plate=2266 Col=15 Row=A"
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Pred. No. 5.1;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Sequence Tagged Connector
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Location/Qualifiers
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Copyright (c) 1993 - 2005 Compugen Ltd
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177
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Maximum Match 100%
Listing first 45 summaries
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                     106 trictitagrecaccitaciaticientificaragaarccentracaccitata 165
                                                                                                                                                                                                                                  GGCACAGGCCCTTCCAACCAGCTCGTGCCCAGAGAACACATGACCGGCATTTCAACCAAT 225
                                                                                                                                                                                     GGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAG 124
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                            5 TATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATC 64
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murtata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
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Anther integrated sequences analysis (Alba) system 101 (11), 1757-1771 (2000) 384 multicapillary system 101 (11), 1757-1771 (2000) 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) 384 multicapillary sequencer. Genome Res. 10 (21), 281-289 (2001) encyclopedia: real-time sequence Custering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Basea; 1 to 402]

S. Vazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osaro, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldaelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chobni, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
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Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L23041A03"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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BY077721
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Best Local Similarity 51.7.
Best Local 75; Conservative
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89 CTTAATGTGATCCCCCCCCCTTTCCTTTCTCCGTAGCCTGACGCGCAGCAGCAGCCGCTTT 148
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Best Local 8
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CV068875
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KEYWORDS
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KEYWORDS
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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Paran, W.J., Pertea, G., Pesole, G., Perceysky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, J., Ringy, B.Z., Kingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Verardo, R., Wagner, L., Wahlested, C., Wang, Y., Watanabe, Y., Verardo, R., Wagner, L., Wahlested, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynhaw-Boris, A., Yanagisawa, M., Yang, I., Yann, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komuo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Srakazume, N., Kagwa, I., Miyazaki, T., Waki, K., Sasaki, D., Shibata, R., Sakai, K., Sakai, P., Shibata, R., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-45-503-9212
Fax: 81-45-503-9212
Fax: 81-45-503-9212
Alzawa, K., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Namm. Genome. 12, 673-677 (2011)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence clustering for construction of a nonredundant cDNA library. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Net Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult male liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="liver"
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Location/Qualifiers
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/strain="C57BL/6J"
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Best Local Similarity 51.73
Matches 75; Conservative
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Gaps

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3 CITATCGTGACAGGACGCCAGCTTCCTGTGTTACCGCAGCCGGACGCAACTCCTTA 62

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348 bp mRNA linear EST 11-DEC-2002
BY338426 RIKEN full-length enriched, whole joints Mus musculus cDNA
EX338426
BY338426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CV068875 931 bp mRNA linear EST 24-AUG-2004 f2_new_chopped.fasta.Contig488 Preamplified custom cDNA library in pCMVsport6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA
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Emiliania huxleyi
Emiliania huxleyi
Bukaryota; Haptophyceae; Isochrysidales; Emiliania.
1 (bases 1 to 931)
Wahlund, T.W., Zhang, X. and Read, B.A.
Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying
Cultures of Emiliania huxleyi
63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                    149 cércaccaderedeaererecres de des de conseceraçes en de consecendos de consecen
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 348)
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/organism="Emiliania huxleyi"
/organism="Emiliania huxleyi"
/organism="Essa"
/strain="1516"
/strain="1516"
/dev_stage="Late log growth phase"
/clone_lib="Preamplified custom cDNA library in
pcWr9port6.1 (ResGen, Invitrogen Inc.)"
/note="Emiliania huxleyi grown in Artificial Seawater
(Guillard's F/2 media)."
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Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
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Pred. No. 8.2;
0; Mismatches
                                                                                                                                                                                                                           123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                       209 GACAGAGCGTCCCGCTTCTCC 233
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Mus musculus
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Gaps .

Length 348; 70; Indels

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AUTHORS

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Mammalia, Burneria; Rodentia; Scilloghachi; Fulloge; Mullhae; Mulliac; Sokazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,T., Osato,N., Saito,R., Suzuki,H., Yananaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Ouackehbush,J., Schrimh,L.M., Kanapin,A., Marsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Gadaterlland,T., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Lenhard,B.,L., Miki,H., Nagashima,T., Namathashi,I.V., Lee,Y., Lenhard,B.,L., Miki,H., Nagashima,T., Namathashi,I.V., Pertea,G., Pertea,G., Pescole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Ring,B.L., Kanachad,R., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Pontius,J.U., Radaji,M., Shimada,K., Sultana,R., Taylor,M.S., Tasadale,R.D., Tomita,M., Verardo,R., Wanger,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wanger,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Hayatsu,N., Hirozane-Kishikawa,T., Yang,Y., Zaudie,R., Kawai,J., Aizawa,K., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Shinagawa,T., Pukuda,S., Hara,A., Hashizum,W., Itoh,M., Kagawa,I., Watanaki,R., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Analysion
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                     /tissue type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 9.2;
0; Mismatches
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/clone="L230014G21"
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Nature 420, 563-573 (2002)
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                     Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Sihongawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Sihonbach, C., Goldbori, T., Baldarali, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schrimm, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousine, S., Dalla, E., Dragani, T. A., Fletcher, C., Gorbani, L.E., Cousine, S., Dalla, E., Dragani, T. A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V. Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Naltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, C., Petrovosky, N., Pillaik, P., Portea, C., Petrovosky, N., Pillaik, P., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Wangi, L., Yuan, Z., Zawai, R., Yang, L., Yuan, Z., Zawai, S., Yang, L., Yuan, Z., Zavolan, M., Shinaki, Y., Hirozane-Kishikawa, T., Yang, Y., Watanabe, Y., Rayatsu, N., Hirozane-Kishikawa, T., Yang, I., Nakawa, I., Miyazaki, T., Waki, K., Kawai, J., Aizawa, K., Shinagawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, R., Savalina, M., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.
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Aizawa.K., Akimura.T., Arakawa.T., Carninci,P., Fukuda,S.,
Hirozane.T., Indeani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
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Fax: 81-45-503-9216
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Tissues were provided by Vassilis Aidinis (Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
acknowledge.
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
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Location/Qualifiers
1. .348
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FEATURES

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Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Gradt, D., Garimond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanaja, A., Kawasawa, Y., Kedalerski, R.M., King, B.L., Konagaya, A., Maltais, L., Marchionni, L., McKenzie, L., MixiH., Nagashima, T., Numata, K., Okido, T., Pevan, W.J., Pertca, G., Pesole, G., Percokkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Povan, W.J., Pertca, G., Ramachandran, S., Ravasi, T., Reed, D. G., Raid, B. Z., Kingwald, M., Sandelin, A., Schneider, C., Sectou, M., Schneider, C., Sectou, M., Schneider, C., Wang, Y., Varado, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yana, Z., Zavolan, M., Zhu, Y., Zimmer, A., Nakanura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sarunishi, A., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Saunishi, A., Yasunishi, A., Y
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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/cell_line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
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                                                          Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
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Genomic Sciences Centers and Genome Spience Laboratory in RIKEN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Okazaki, Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 CTTAATGTGATCCCCCCCCCTTTCCTTTCTCCGTAGCCTGACGCGGCAGCAGCCGCTTT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Division of Experimental Animal Research in Riken contributed to
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/clone_lib="RIKEN full-length enriched, whole joints"
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Ribases I to 355)

Nikaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yamanaka, I., Kajodo, I., Tomaru, Y., Hasegawa, Y., Mogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Haralo, S., Dalla, B., Brasic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T.A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawasawa, Y., Lenhard, B., Lowns, P.A., Maglott, D.R., Numatcais, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G., Narchina, L., Marchinni, L., McKenzie, L., Miki, H., Magashima, T., Numatcais, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Pontius, J.U., Qi, D., Ramachandran, S., Sultana, R., Takenaka, Y., Walserska, M., Shimada, M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhime, M., Yang, Y., Watanabe, Y., Karakawa, T., Kono, H., Nakamura, M., Sato, K., Sato, K., Shiraki, Y., Kono, H., Nakamura, M., Sato, K., Shiraki, Y., Waterston, R., Lander, B.S., Rogers, J., Birney, E. and Haysshizaki, Y. Rangawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Lander, E.S., Rogers, J., Birney, E. and Haysshizaki, Y. Rang, M., Radawa, T., Rangawa, T., Rangawa, T., Rangawa, T., Rangawa, T., Rangawa, T., Sakai, W., Barney, E. and Haysshizaki, Y. Rasaki, D., Sasaki, Y., Sas
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                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Alzawa,Y., Akimura,T., Arakkwa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
                                                                                                                                 CTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
                                                                       Gaps
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0
      DB 5; Length 354;
                                                                    70; Indels
                                                                0; Mismatches
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   Score 33;
Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 GACAGAGCGTCCCGCTTCCCTCTCC 260
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Mus musculus
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Query Match
Best Local Similarity 51.7%;
Matches 75; Conservative
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BY340467
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Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare full-length cDNA libraries for trapper sequencer. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system--184-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA convecting for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kondo, S.,
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Sauvki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T.,
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/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 9.2;
0; Mismatches
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9.2;
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Mus musculus
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Best Local Similarity 51.7%;
Matches 75; Conservative (
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Mammalia burneria; Rodentia; Scurrognath; Muridae; Murinae; Muse Bonderia; Loado, R. Kasukawa T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, N., Saito, R., Buzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T. Baldarelli, R., Hill, D. P. Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanabin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Batalov, S., Beisel, K.W., Brake, J.A., Bradt, D., Brusic, V., Ghothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboddi, M., Gissi, C., Godzik, A., Gaugh, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Kurochkin, I.V. Lee, Y., Lehdard, B., L., Wons, P.A., Maglott, D. R., Nantais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Petrovsky, N., Pellai, R., Pontius, J.U., Qi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B. Z., Ringwald, M., Saltana, R., Takenaka, Y., Wallang, L., Wandestedt, C., Wang, Y., Watanabe, Y., Arakawa, T., Rudda, S., Harah, H., Hashizume, W., Inctan, K., Sarato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Shiraki, Y., Malyashizaki, Y., Arakawa, T., Miyazaki, A., Hashizume, W., Inctan, K., Saration, R., Shiragawa, A., Yasunishi, A., Yoshino, W., Malested, Y., Sasati, D., Shibata, K., Shiraky, B., and Hayatsu, B., Wasunishi, A., Yoshino, W., Materston, R., Lander, E.S., Rogers, J., Birney, E., and Hayatsuk, Y., Yashin, Y., Yashi
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
                                                                                   3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
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Mus musculus
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King B.L., Konagaya, R.,
Kurochkin, I.V., Lee, Y., Leedracki, R.M., King B.L., Konagaya, R.,
Kurochkin, I.V., Lee, Y., Lendard, B.L., Mons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Oxido, T., Paran, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, Ju., Reid, J., Ring, B.E., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Warcanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carnini, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Itoh, M., Kagawa, I., Miyazaki, A., Sasaki, W., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 [ull-length cDNAs
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
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/clone_lib="RIKEN full-length enriched, whole joints"
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/db_xref="taxon:10090"
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JOURNAL MEDLINE PUBMED COMMENT

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18.6%; Score 33; DB 5; Length 360; 51.7%; Pred. No. 9.2; ive 0; Mismatches 70; Indels

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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia: Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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BY083658 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630044L13 5', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, whole joints"
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/organism="Mus musculus"
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Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okio,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pointius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandellin,A., Schneider,C., Semple,C.A., Setou,M., Shinada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinaqawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
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Fax: 81-45-50-321.

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozanc, T., Imocani, K., Ishli, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagani, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAS Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

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cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Labbractory in RIKEN.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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/clone_lib="RIKEN full-length enriched, 10 days neonate
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51.7%; Pred. No. 9.2;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .371
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 420, 563-573 (2002)
22354683
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Best Local Similarity
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/clone lib="Talri"
/note="Vector: Lambda ZapII; mass excised in plasmid
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site I: EcoRI; Site 2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avrl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ620008 621 bp mRNA linear EST 28-JUN-2002 Tabr1138G03F Tabr1 Triticum aestivum cDNA clone Tabr1138G03F, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (204) 983-2340

Fax: (204) 983-4604

Email: scloutier@expr.gc.ca
was cloned directionally, not all sequences generated with reverse primer where from the 5' end (same with forward primer and 3'end).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum
Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                           chrandrehencecececerriteinnereceraseeraseeraseeraseeraseera
                                                                                                                                                                                                                                                          63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                       109 CCTCACCAGCTCGCACTCTCCTCGGGGCCGCACGGCTCGCCGTGCCCCTGCCCACCACCACGG 168
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                                                                                                                                                               3 CTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloudier, S., Dong, G. and Walsh, A.
Wheat functional genomics - Thatcher Lr1 cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                  ö
                                                                     Length 611;
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                                                                                                               70; Indels
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51.7%; Pred. No. 9.3;
iive 0; Mismatches 70
                                                                     DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="Thatcher Lr1"
/db xref="taxon:4565"
/clone="Talr1138G03F"
/tissue_type="Leaf tissue"
/dev stage="14 Days old"
/lab_host="E, coli XLOLR"
constructed by Yulan Piao."
                                                                   Score 33; DB 'Pred. No. 9.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      169 GACAGAGCGTCCCGCTTCCCTCTCC 193
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Plate: 138 row: G column: 03
Seq primer: M13 Forward.
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BQ620008.1 GI:21625087
                                                                   Query Match
Best Local Similarity 51.7%;
Matches 75; Conservative
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Best Local Similarity
Matches 75; Conserv
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TITLE
JOURNAL
COMMENT
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BQ620008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 611)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genefics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 188 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dI)
                                                                171 GCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTGGCGTGCCCTGCCCTGCCACCACGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                   TCGGAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0991 row: A column: 12
Seg primer: M13 Reverse
High quality sequence stop: 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="NIA:B0991A12 IMAGE:30480971"
dev stage="Unfertilized Egg"
lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
strain="C57BL/GJ"
db_xref="nials": B0991A12-5"
db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 11 (9), 1553-1558 (2001)
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/organism="Mus musculus"
                                                                                                             123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                          231 GACAGAGCGTCCCGCTTCCCTCTCC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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AUTHORS
TITLE
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MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                  RESULT 12
CF916169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mutinae; Mus. 1 (bases 1 to 635)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Puderwood,K., Steptoe,M., Theising,B., Allan,M., Bowers,T., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                               93 CCTCACCAGCTCGCACTCTCCTCGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCACGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                               3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
                                                                                                                                                                                                                                                                                          33 critaardrearccccccccrrrccrrrccrrccraeccreaceceecaecaecrir
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                 DB 7; Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                          9.3;
                                                                                          18.6%; Score 33; DB 51.7%; Pred. No. 9.3; ive 0; Mismatches
constructed by Yulan Piao."
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High quality sequence stop: 305.
Location/Qualifiers
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/clone="IMAGE:2395039"
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Mus musculus
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/strain="C57BL"
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                                                                                                                             Local Similarity 51.7% tes 75; Conservative
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                                                                                                 Query Match
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DEFINITION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site 2: Not1; Mouse cDNA project by the Laboratory of GeneLics, National Institute on Asing (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                EST 05-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                         CF913548
B0950D02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0950D02 IMAGE:30477061 5', mRNA sequence.
                        CCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                495 cgacarctrocoronicatorologoggangganggangrocologogaan 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="niaEST:80950D02-5"
/db_xref="taxon:10090"
/clone="N1A:80950D02 IMAGE:30477061"
/dev_stage="Unfertilized Egg"
/lab_hoste="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 11 (9), 1553-1558 (2001)
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Plate: B0950 row: D column: 02
Seg primer: M13 Reverse
High quality sequence stop: 624
POLYA=No.
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                                                                                                                                                                                                       555 CGGCACGAGGCGCACAGAAGGCAA 579
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                                                                                                                                                         141 TCGCGCCTATAAATACAGCCCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF913548
CF913548.1 GI:38184750
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                                                                                                                                                                                                                                                                                                                          RESULT 14
CF913548
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TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
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Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACA."
                                                                                                ORIGIN
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· 0 Query Match 18.6%; Score 33; DB 2; Length 635; Best Local Similarity 51.7%; Pred. No. 9.3; Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps

63 TCGGAACAGGACGCCCTCCATATCAGCCGCGGTTATCTCATGCGCGTGACCGGACACG 122

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Search completed: October 24, 2005, 21:53:24 Job time : 1285.71 secs 158 GACAGAGGGTCCCGCTTCCCTCC 182

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Abl19245 Drosophil
Abl19244 Drosophil
Ada01209 Human col
Ad45695 Bacterial
Abd13766 Pseudomon
Ach89781 Human gen
Acs17480 DNA encod
Acs151490 Pseudomon
Aca13495 Prokaryot
Ad556860 Bacterial
Abd13493 Pseudomon
Abd13493 Pseudomon
Abd13431 Pseudomon
Abd13533 Pseudomon
                                                                                                                       Aax06989 Human neu
Abk50730 CDNA enco
Aax06988 Human neu
Abk90731 cDNA enco
Adt43165 Bacterial
Aca45469 Prokaryot
Ad127170 Human gen
Ada3092 Human LFN
Ada6376 Human LFN
                                                                                                                                                                                                            Adb72830 Human LFN
Acn43958 Human gen
Aac23731 Human sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; OpIE2 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Madden K,
                                                                                                                                                                                                                                                           ALIGNMENTS
                            ADT45695
ABD13766
ACH89781
AAS70780
AAS51490
ACA19456
ADS56860
                                                                                             ABD13493
ABD13719
ABD13633
AAX06989
ABK90730
AAX06988
ABK90731
ADT43165
ACA5469
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ADA03092
ADA6376
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ACN43958
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26-JUL-2002; 2002US-0396617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
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                                                                                                                                                                                                                                                                                                                                                               OpIE2 promoter DNA sequence.
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75839
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FRIMPONG K.
FRANKE K E.
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                             ADQ48575;
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(FRIM/) r
(FRAN/)
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(BENN/)
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                                                                                                                                                                                                                                                                                      RESULT 1
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  Add4855 OpiE2 pro
Ad64857 O. pseudo
Ad64859 Viral vec
Ad48576 Viral vec
Ada02474 Human col
Ab12503 Drosophil
Ab127503 Drosophil
Ab12800 Drosophil
Ab18800 Drosophil
Ad18800 Drosophil
Ad18800 Drosophil
Ad18800 Brosophil
Ad47065 Bacterial
Ad47085 Bacterial
Ad44088 Beseudomon
Ad88938 Oligonucl
Ad889483 Oligonucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abk31430 Signal tr
Abl70389 Chemicall
Aas61341 Human gen
Adf83430 Bread whe
                                                                ; Search time 193.335 Seconds (without alignments) 5419.578 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                       1 gtcttatcgtgacaggacgc......gcccgcaacgatctggtaaa
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                     4390206 segs, 2959870667 residues
                                                                                                    US-09-896-888A-1_COPY_351_527
177
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                                                                October 24, 2005, 18:39:18;
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Maximum Match 100%
Listing first 45 summaries
                                              nucleic search, using sw model
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AAV62487
AAL61306
ADQ48539
ADQ48576
AAA02474
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ABL27502
ABL18800
AAD64735
ADT47065
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ABD14088
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AAS61341
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Gapop 10.0 , Gapext 1.0
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length: 200000000
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Match Length DB
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Franke KE;

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                                                                         portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCGGAACAGGACGCGCCTCCATATCAGCCGCGGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 474
                                                                                                                            undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a precombinant virus, generating replication-defective particles, preventing the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpiE2 promoter that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression vectors for transforming insect cells from disparate lines - useful to express heterologous DNA, e.g. to allow study of gene
                                                     The invention comprises a nucleic acid molecule consisting of all or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGGCCCCGCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGGCCCCGTCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter.
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                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 177; DB 12; Length 560; 100.0%; Pred. No. 2.6e-48;
                                                                                                                                                                                                                                                                                                                                          Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pseudotsugata; polyhedrosis virus.
                 Disclosure; Fig 16; 555pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ion transport peptide hormone; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA
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(first entry)
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Matches 177; Conservative
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19-JAN-1999
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that comprises: (1) prokaryottic origin of replication; (11) insect care that the comprises: (1) prokaryottic origin of replication; (11) insect care promoter having homology to, and capable of functioning as, an immediate carly baculovirus promoter; (11) prokaryottic promoter sequence, and (1v) selectable marker capable of conferring resistance to a bleomycin. Or capable of conferring resistance to a bleomycin. Or capable of conferring respectively. The vectors can be used to stably transform (especially insect) cells with heterologus DNA, useful to allow expression and direct expression of heterologus gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologus melanotransferring, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell inse from disparate species, allowing screening of lines for optimum post-translational modification of particular proteins. Shuttle vectors (urther comprising DNA transposable elements defining a transposon can be used to optimise heterologus protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 GretrarcereacadeaceceaecrecerererrecrarececaeceaececaAcreer 410
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tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CGAGGCGCCCGTCCCGCTTATCGCCCTATAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                 This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCTCATGCGCGTGACCGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 564 BP; 147 A; 160 C; 116 G; 141 T; 0 U; 0 Other;
expression and produce commercially important proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p2ZOp2F expression vector for insect cells.
                                       Claim 10; Page 82; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL61306 standard; DNA; 2773 BP
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16-NOV-2001; 2001US-0331575P.
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NIELSEN F S.
BRATT T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL61306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KLYS/)
(NIEL/)
(BRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHAR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL61306
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portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombining at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and etcher of the invention replicates in prokaryotic and entaryotic cells. The nucleic acid of the invention is useful for constructing a recombinating/simbibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that was used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCACGTGACCGGACA 470
                                                                                                                                                                                                                                      Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGGCCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCCCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GICTIAICGIGACAGGACGCCAGCTICCIGIGITGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viral vector-related plasmid pIB/V5-His-DEST recombination region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 5038;
                                                                                                      Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Score 175.4; DB 12 99.4%; Pred. No. 1.5e-47; vative 0; Mismatches 1;
                                                                                                      Madden K,
                                                                                                                                                                                                                                                                                                                                                                          Example 18; Page 395-403; 555pp; English.
                                                                                                      Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ48576 standard; DNA; 141 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2003; 2003WO-US022437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 99.4 ses 176; Conservative
                                                                                                      Bennett RP, Welch PJ,
                                                                                                                                                                          WPI; 2004-132944/13.
   (FRIM/) FRIMPONG K.
(FRAN/) FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004009768-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ48576
       THE SECTION OF THE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis factor alpha (TNF, TNFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is p220p2F expression vector for insect cells. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 GICTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCGGGACGCAACTCCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 474
                                                                                                                                                                                                                                   New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGGCGCCCCTCCCGCTTATCGCCCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475 CGAGGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GICTIAICGIGACAGACGCCAGCTICCIGIGITACTAACCGCAGCCGGACGCAACTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
                                                                                                      Mouritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 177; DB 9; Length 2' Best Local Similarity 100.0%; Pred. No. 3.86-48; Indels
                                                                                                   Voldborg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viral vector-related plasmid - pIB/V5-His-DEST
                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 195-196; 196pp; English,
                                                                                                   Bratt T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ48539 standard; DNA; 5038 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-039617P.
19-NOV-2002; 2002US-042731P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
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BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                   Klysner S, Nielsen FS,
(VOLD/) VOLDBORG B. (MOUR/) MOURITSEN S.
                                                                                                                                                                   WPI; 2003-449558/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADDEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004009768-A2.
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ABL18801 standard; DNA; 1268 BP.
 98US-0105877P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 TAAGATCGNGCC 26
                                                                  Williams LT, Escour-
Reinhard C, Glese K, F
Drmanc R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                        Escobedo
                                   (CHIR ) CHIRON CORP.
                                                                                                                                                                              WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
   27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL18801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                     portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of presence of one or more proteins active in lambda recombination. The presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                              Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; coestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                          The invention comprises a nucleic acid molecule consisting of all or a
                                                                                                                                                                              Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%; Score 41; DB 12; Length 141; 100.0%; Pred. No. 0.0014; Live 0; Mismatches 0; Indels
                                                                                                                                                                              Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATCGCGCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                                                                            Madden K,
                                                                                                                                                                              Harwood S,
                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 17; 555pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0085426P.
98US-0085537P.
98US-0085696P.
98US-0105234P.
03-JUN-2003; 2003US-0474940P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA02474 standard; cDNA; 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                   INVITROGEN CORP.
                                                                                                                                                                            Sennett RP, Welch PJ,
                                                  BENNETT R P. WELCH P J. HARWOOD S.
                                                                                                                                                                                                               WPI; 2004-132944/13.
                                                                                                     (MADD/) MADDEN K.
(FRIM/) FRIMPONG K.
(FRAN/) FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                  (WELC/)
(HARW/)
                                                   BENN/)
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76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test asmaple deterived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides some be used in a method for detectining differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GACGCCAGCTTCCTGTGTTACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 GGCGTCNAANCCACCTTCCCTTCGTCTCCGGCTCCGCGTTCAGGGAGCGACTGTCCT 38
                                                                                                  Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of premetastatic or metastatic cancervous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                      Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
    J, Innis MA, Garcia PD, Sudduth-Klinger Randazzo F, Kennedy GC, Pot D, Kassam A; Crkvenjakov R, Dickson M, Drmanac S, Lab Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                negative breast cancer, lung cancer, and colon cancer
Garcia PD,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
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                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher exaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABR2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
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  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.8; DB 4; Length 1342; Pred. No. 5.7; 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1342 BP; 324 A; 347 C; 372 G; 299 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          791 ĠTTGGĊACATTGĠĊĊATAĊAAATCĊŢĊAAĠTCĊCAĠAAAĠTÄĊAAĠ 836
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                                                                                           Claim 1; SEQ ID NO 33982; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                  from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ID ABL27502 standard; DNA; 3448 BP
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 55...
Thea 59; Conservative
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ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
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                                                                                                                                                              Venter JC, Adams M,
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ABL27503
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1667 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 1608
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                  sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                     Score 30.8; DB 4; Length 3448; Pred. No. 7.1; 0; Mismatches 47; Indels 0
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                                                                                                                    Sequence 3448 BP; 894 A; 817 C; 801 G; 936 T; 0 U; 0 Other;
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11-JUL-2000; 2000US-00614150.
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55.7%;
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Best Local Similarity
<sub>(</sub>Matches 59; Conserva
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1667 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel recombinant carcinoma-associated protein (CAP) useful for screening a bioactive agent capable of binding to carcinoma associated (CA) protein and for evaluating the effect of a candidate carcinoma drug. The invention also describes the use of novel compositions for use in screening methods and provides compositions and methods associated with altered expression of TBX21 in cancer. Sultable cancers which can be diagnosed or screened by the invention includes acinar cell carcinoma, fibrosarcoma, Kaposi's sarcoma, breast cancer and the present sequence is human carcinoma-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel recombinant carcinoma-associated protein such as mouse or human MRX1 protein, useful for screening a bioactive agent capable of binding to carcinoma associated protein, and for evaluating the effect of a candidate carcinoma drug.
                                                                                                                                                                                                                                                                                                                              Carcinoma-associated protein; CAP; acinar cell carcinoma; fibrosarcoma;
Kaposi's sarcoma; breast cancer; Hairy cell leukaemia; human; ds.
17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29169 BP; 5725 A; 7553 C; 7224 G; 8641 T; 0 U; 26 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 29169;
                                                                                                    1607 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                     GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%; Score 30.8; D
61.0%; Pred. No. 12;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                               Human carcinoma-associated (CA) gene TBX21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, SEQ ID NO 4; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9042 cccccrccccccccccccc 9063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 GGACGCCCTCCATATCAGCCG 92
                                                                                                                                                                                         AAD64735 standard; DNA; 29169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2000; 2000US-00747377.
02-MAR-2001; 2001US-00798586.
08-NOV-2001; 2001US-00052482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2002; 2002US-00105613
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-874605/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 50, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MORR/) MORRIS D W.
                                                                                                                                                                                                                                                                                                                                                                                                                     US2003099963-A1.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                              11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                   11
                                                                                                                                                                                                                            AAD64735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Gaps

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Length 1404;

DB 13; 29;

17.3%;

Conservative

Similarity

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Best Local Simi
Matches 48;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                             Recombinant DNA construct, transformed plant; improved plant property; cold tolerance, heat tolerance, drought tolerance, herbicide, osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polymucleotide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 45503; 122pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen X,
                                                                         ADT47065 standard; cDNA; 1404 BP.
                                                                                                                                                                                            Bacterial polynucleotide #21816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003; 2003US-00369493
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                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-061375/06.
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SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN X.
                                                                                                                                                       02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2003
                                                                                                                ADT47065;
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HINK/) (SLAT/) (CHEN/) (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y,
                                    RESULT 12
                                                       ADT47065
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encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                                                                523
                                                                                                                                                                                                                                                                                                                isoprenoid biosynthesis; ss; isopentenyl diphosphate; IPP; dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll; haeme; yield.
                                                       99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCCGCTTATCGCGCCCTATAAATACAG
                                                                                464 Accechadedecidadacenecedanoneanecidececinecedecidenineegecaage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a polynucleotide (or its complement, protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B, Glazebico. ...
, Provart N, Ricke
                                                                                                                                                                                                                                                                                              Plant isoprenoid biosynthesis-associated DNA #6.
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(atagiri F, Kreps J, Moughamer T,
Score 30.6; DE Pred. No. 6.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 563; 117pp; English
                                                                                                                                                                                                             ВР
                                                                                                                                       524 ACCGCGACGATCTGGAA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001; 2001US-0325277P.
04-APR-2002; 2002US-0370620P.
04-APR-2002; 2002US-0370743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2002; 2002US-00259194.
                                                                                                                                                                                                            ADI45632 standard; DNA; 657
                                                                                                            159 CCCGCAACGATCTGGTA
                                                                                                                                                                                                                                                                    22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LANGE B M.
GHASSEMIAN M.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KREPS J.
MOUGHAMER T.
PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-090562/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004010815-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lange BM,
Goff SA,
Zhu T;
                                                                                                                                                                                                                                        AD145632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAZ/)
(GOFF/)
(KATA/)
(KREP/)
(MOUG/)
(PROV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GHAS/)
(BRIG/)
(COOP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHUT/)
                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                ADI45632/
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providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPFO at sequance.

Sequence 1404 BP; 236 A; 489 C; 454 G; 225 T; 0 U; 0 Other;

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expression cassette, and atransporter, ansor certicularity concerned cassette. The polypeptides and polynucleotides include those associated with the biosynthesis of isopentenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid parental corporation of the biosynthesis of short-chain plastid preparates, the biosynthesis of short-chain plastid carotenoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of tocopherols, physosterol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of monterpenes and sesquiterpenes, protein prenylation, and biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polymucleotides. The polymucleotides are useful for producing transpence plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a loss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a loss, and probes. Note: The sequence date for this patent did not form pair of produce a corn pair produce a produce and probes. Note: The sequence date for this patent did not form bait of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                            format directly from USPTO at sequence.html?DocID=20040010815. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTTCCCGCTTATCGCGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is an isoprenoid biosynthesis- associated DNA included in the sequence
listing but not mentioned anywhere else in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
comprising the polynucleotide, a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 16.9%; Score 30; DB 12; Length 657; I Similarity 53.4%; Pred. No. 8.9; 63; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 657 BP; 109 A; 257 C; 178 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa polynucleotide #12692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-615309/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1998;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapper controlled targets for diagnosis and prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABD1767 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 CCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 CCAAAATAGCCGCTCGATCTCTCGGCGAAGTGACGGGGCACCTGGCGAGCGCATTGCCCC 355
useful as molecular targets for diagnostics, prophylaxis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicting responsiveness of a subject with breast cell proliferative disorder, useful for treating or differentiating breast cell proliferative disorders comprises analyzing methylation pattern of a genomic DNA from the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Model F;
Marx A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 16.9%; Score 30; DB 11; Length 1710; Local Similarity 57.4%; Pred. No. 11; hes 54; Conservative 0; Mismatches 40; Indels
                     pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1710 BP; 380 A; 455 C; 526 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maier S, Martens J,
Schmitt M, Look MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 TCGCGCCTATAAATACAGCCCGCAACGATCTGGT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 recececerchaerecrecarecaecerecheer 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide of the invention SEQ ID NO:401.
                                                         Disclosure; SEQ ID NO 12692; 455pp; English
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Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                           seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002; 2002DE-01045779.
07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS89385 standard; DNA; 3107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foekens J, Harbeck N,
Nimmrich I, Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-348468/32
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The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comparising the methylation pattern of a target mucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligonmers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for the credicting the responsiveness of a subject with a cell proliferative disorders is a therapy. The present sequence is used in the exemplification of the invention.
                           Claim 25; SEQ ID NO 401; 104pp; English
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Sequence 3107 BP; 823 A; 120 C; 814 G; 1350 T; 0 U; 0 Other;

6 ATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCG 65 Gaps ö 'Match 16.9%; Score 30; DB 13; Length 3107; Local Similarity 50.7%; Pred. No. 13; les 72; Conservative 0; Mismatches 70; Indels (Query Match Best Loca Matches

2079 AACGCGAAACCACCGCTCCTCCTCCAACCGCCGCGAATAACCTCAACGCC 2020

qq ò g ò

Search completed: October 24, 2005, 18:58:05 Job time : 199.335 secs

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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database

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Sequence 60, Appl
Sequence 127, Appl
Sequence 127, App
Sequence 2538, Ap
Sequence 2538, Ap
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                           Sequence 25442, A Sequence 38495, A Sequence 38494, A Sequence 25411, A Sequence 54126, A Sequence 54126, A Sequence 56107, A Sequence 7296, A Sequence 7296, A Sequence 50101, A Sequence 52916, A Sequence 52916, A Sequence 52916, A Sequence 52916, A Sequence 22, Appl Sequence 22, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 177; DB 9; Length 462; 100.0%; Pred. No. 2e-54; ive 0; Mismatches 0; Indels
24 US-10-939-107-60
21 US-10-622-088-89
22 US-10-622-088-127
23 US-10-622-088-127
24 US-10-622-088-149
25 US-10-156-761-1
26 US-10-156-761-1
26 US-11-097-143-2542-8561
26 US-11-097-143-2542-8561
26 US-11-097-143-2542-8561
26 US-11-097-143-2542-8563
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20 US-10-97-143-25413
20 US-10-275-311A-10
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20 US-10-275-311A-10
21 US-10-275-312A-133
21 US-10-425-112-65944
21 US-10-425-112-65944
21 US-10-425-122A-7326
22 US-10-369-493-32534
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US-10-215-862-22

US-10-215-862-22

US-10-315-862-22

US-11-035-787-22

US-09-817-665-5
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Patent No. US20020116723A1
GENERAL INFORMATION:
GENERAL INFORMATION:
HAPLICANT The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REPERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
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Best Local Similarity 100.
Matches 177; Conservative
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Sequence 126, App
Sequence 1, Appli
Sequence 60, Appl
Sequence 60, Appl
                                                                                                                                                                                                                                    October 24, 2005, 20:18:24; Search time 361.161 Seconds (without alignments) 4044.488 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gtcttatcgtgacaggacgc......gcccgcaacgatctggtaaa 177
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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20: /cgn2_
                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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21 US-10-622-088-126
9 US-09-896-888A-1
17 US-10-295-074-60
21 US-10-846-911-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9772363 segs, 4126298632 residues
                                                                                                                                                                                                                                                                                                                                                                      US-09-896-888A-1_COPY_351_527
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
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Gaps

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APPLICANT: The University of British Columbia
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                                                                                                                                                                                                                                   TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                   310 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 369
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                                                                                                                                                                                                                                                                                                                                                                                                             CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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GREAL INCOMMATION:
APPLICANT: Bennet, Robert P.
APPLICANT: Walch, Peter J.
APPLICANT: Wadden, Knut
APPLICANT: Madden, Knut
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: ECT/US03/22437
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-38
PRIOR FILING DATE: 2003-07-18
PRIOR PELING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-38
PRIOR PELING DATE: 2003-07-38
PRIOR FILING DATE: 2003-07-38
PRIOR PELING DATE: 2003-07-38
PRIOR PELING DATE: 2003-03-34
PRIOR PELING DATE: 2003-05-34
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; Sequence 126, Application US/10622088
; Publication No. US20040219516A1
; GENERAL INFORMATION:
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ORGANISM: Unknown
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Sequence 1, Application US/0989688BA Patent No. US20020116723A1 GENERAL INFORMATION:

US-09-896-888A-1

RESULT 3

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351 Greffarcereacacaccacericereferrecraaccccacceacccaacteer 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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Sequence 60, Application US/10295074

Publication No. US20030185845A1

GENERAL INFORMATION:
APPLICANT: Pharmexa A/S

TITLE OF INVENTION:
TITLE OF INVENTION NUMBER: US/10/295,074

CURRENT APPLICATION NUMBER: US/10/295,074

CURRENT FILING DATE: 2002-11-15

NUMBER OF SEQ ID NOS: 60

SOFTHARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                              Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 177; DB 9; 100.0%; Pred. No. 2e-54;
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-4
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Orgyia pseudotsugata
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OTHER INFORMATION: ECORI site
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LOCATION: (625).. (630)
OTHER INFORMATION: ClaI site
FEATURE:
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NAME/KEY: misc_recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.0
Matches 177; Conservative
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI
FEATURE:
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NAME/KEY: misc recomb
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LENGTH: 2773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2773;
       OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                          FEATURE:
NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                   NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_recomb

LOCATION: (2551)..(2556)

OTHER INFORMATION: Apals site

US-10-846-911-60
                                                                                                                                                                                                                                                                                                                                                     LOCATION: (593). (598)
OTHER INFORMATION: BamHI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
                                                                                                                                                                  LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (629)..(634)
OTHER INFORMATION: Clai site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: Pet1 site
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OTHER INFORMATION: NCOI Site
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OTHER INFORMATION: Aval site
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LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval,
                                                                                                                                         NAME/KEY: misc_recomb
LOCATION: (573)..(578
                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc recomb
LOCATION: (593)..(598
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LOCATION: (2204)..(22
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LOCATION: (2284)..(22)
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LOCATION: (629)..(634
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US-10-939-107-60
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US-10-846-911-60

US-10-846-911-60

Sequence 60, Application US/10846911

Publication No. US2040258660A1

GEPERAL INFORMATION:

APPLICANT: KIVSNER, Sten

APPLICANT: WISLERN, Finn Stausholm

APPLICANT: WOURTYSEN, Soren

TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

FILE REFERENCE: 67454-2018

CURRENT APPLICATION NUMBER: PCT/DK02/00764

PRIOR FILING DATE: 2004-05-14

PRIOR FILING DATE: 2002-11-16

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.1

SEQ ID NO 60

LENGTH: 2773

TAPE: 2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 CGAGGCGCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
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100.0%; Pred. No. 2.6e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
COTHER INFORMATION: Apals site
US-10-295-074-60
                                                                                         NAME/KEY: misc recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: ApalI site
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ORGANISM: Artificial sequence
FEATURE:
                          LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
                                                                                                                                                          FEATURE:
NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: P&LI site
                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 177; Conservative
NAME/KEY: misc recomb
LOCATION: (629)..(634
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61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGGTTATCTCATGCGCGTGACCGGACA 120
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                                                                                              415 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGCGTGACCGGACA 474
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                                                                                                                                                                                                                                                                                                                                     121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                             475 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 89, Application US/10622088

Publication No. US20040219516A1

GENERAL INPOMENTION:
APPLICANT: Welch, Feter J.
APPLICANT: Welch, Peter J.
APPLICANT: Wadden, Knut
APPLICANT: Frameon, Kenneth
APPLICANT: Frameon, Knut
APPLICANT: Frameon, Knut
APPLICANT: Frameon, Knut
APPLICANT: Frameon, Knut
CURRENT APPLICANT: Frameon, Knut
APPLICANT: MUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/396,617
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/426,496
PRIOR APPLICATION NUMBER: US 60/426,496
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR APPLICATION NU
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US-10-622-088-127
i Sequence 127, Application US/10622088; Publication No. US20040219516A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.43
Matches 176; Conservative
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APPLICANT: Pedersen, Hans Rudolf
APPLICANT: Ebert, Bjarke
APPLICANT: Ebert, Bjarke
APPLICANT: Pedersen, Louise Henriette
APPLICANT: Pedersen, Louise Henriette
TITLE OF INVENTION: Novel Application of Vaccination Against TNF-alpha
FILE REFERRINCE: 674542-2020
CURRENT APPLICATION NUMBER: 05/10/939,107
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: FCT/DK03/00147
PRIOR PALICATION NUMBER: FCT/DK03/00147
PRIOR PLING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 177; DB 24; Best Local Similarity 100.0%; Pred. No. 2.6e-54; Matches 177; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_recomb
LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc_recomb

) LOCATION: (2551)..(2556)

) OTHER INFORMATION: ApaLI site

US-10-939-107-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: Pstl site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_recomb
LOCATION: (2284).. (2289)
OTHER INFORMATION: Aval site
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc recomb
LOCATION: (629)..(634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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2515 cerreadecercercaceatrere 2491
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                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis
SOFTWARE: Patentin version 3.2
SEQ ID NO 149
LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.2<sup>§</sup>
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (145)..(276)
US-10-622-088-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3138)
US-10-156-761-2538
                                                                                                       ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-156-761-2538/c
                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-10-156-761-1
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Sequence 149, Application US/10622088

Publication No. US2040219516A1

GENERAL INFORMATION:
APPLICANT: Bennett, Robert P.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Franke, Kenneth
APPLICANT: BOG 1942.545001, 18
FILE REFERENCE: 0942.545001, 18
FRIOR APPLICATION NUMBER: US 60/427,231
FRIOR APPLICATION NUMBER: US 60/426,496
FRIOR FILING DATE: 2002-07-18
FRIOR FILING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: US 60/456,496
FRIOR APPLICATION NUMBER: US 60/456,496
FRIOR APPLICATION NUMBER: US 60/47,231
FRIOR APPLICATION NUMBER: US 60/476,496
FRIOR APPLICATION NUMBER: US 60/476,496
FRIOR APPLICATION NUMBER: US 60/476,940
FRIOR FILING DATE: 2003-06-03
FRIOR FILING DATE: 2003-06-03
FRIOR FILING DATE: 2003-06-03
FRIOR FILING DATE: 2003-06-03
                                                                                         APPLICANT: Frimpong, Knuc

APPLICANT: Frimpong, Kenneth

APPLICANT: Frimpong, Kenneth

APPLICANT: Franke, Kenneth E.

TITLE OF INVENTION: Viral Vectors Containing Recombination Sites

FILE REFERENCE: 0942.5450007

CURRENT APPLICATION NUMBER: US/10/622,088

CURRENT FILING DATE: 2003-07-18

PRIOR PILING DATE: 2003-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR PLING DATE: 2002-07-18

PRIOR PPLICATION NUMBER: US 60/398,617

PRIOR PPLICATION NUMBER: US 60/427,231

PRIOR APPLICATION NUMBER: US 60/427,231

PRIOR PPLING DATE: 2003-01-19

PRIOR PPLING DATE: 2003-01-19

PRIOR PPLICATION NUMBER: US 60/474,940

PRIOR PPLING DATE: 2003-03-24

PRIOR PPLING DATE: 2003-03-06-03

NUMBER OF SEQ ID NOS: 165

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.2%; Score 41; DB 21; L 100.0%; Pred. No. 0.00011; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (141).. (148)
OTHER INFORMATION: n may be any nucleotide
US-10-622-088-127
Bennett, Robert P.
Welch, Peter J.
Harwood, Steven
Madden, Knut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-622-088-149
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2575 cerecaecedaecedaecedecerecerreardareaecrreaerredecreeaecede 2516
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
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OTHER INFORMATION: Recombination region of pIB/V5 His DEST
                                                                                                                                                                                                                                                                                                                                                                                                                       137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CITATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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                                                                                                                                                                                                                                                                                                Query Match 23.2%; Score 41; DB 21; I
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 32.2; DE 61.2%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squence 5338, Application US/10156761

Squence 5338, Application US/10156761

GENERAL INFORMATION:
APPLICANT: OWINEA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRAY, YOSHIYUKI
APPLICANT: SHIRAY, YOSHIYUKI
APPLICANT: MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFREENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
SROID NO 2538
SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
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Gaps

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APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: vet al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: (0/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 2000-01-12
PRIOR PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR PRIOR DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR PRIOR PRIOR DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGCGACACGAGGCGCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGCACGCACTCCTTATCGGAACAGGACGC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 GGCAGCTGCGCNCCAGGTGGCTGTCCCACGCCGGTCTCCGCGCCCTGCCCCGGTGCGCGGGT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 gécercinanceacerrecerresreres en construción de contra de contr
                                                                                                                                                                                            FEATURE:

NAME/KEY: misc_feature

LOCATION: 41, 6, 29, 88, 91, 146, 218, 378, 413, 482, 485, 500, 508, LOCATION: 531, 577, 585, 623, 637, 642, 651, 662, 697, 704, 724, 10CATION: 531, 778, 835, 837, 839, 842, 852, 868, 882, 884, 885, 891, 10CATION: 892, 899, 901

COTHER INFORMATION: n = A,T,C or G

US-10-779-543-8561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.5%; Pred. No. 0.29;
Matches 68; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.4%; Score 30.8; DB 26;
55.7%; Pred. No. 0.83;
live 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25442, Application US/11097143 Publication No. US20050208558A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GCTTATCGCGCC 147
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Best Local Similarity 55.77
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 TAAGATCGNGCC 26
                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-097-143-25442
     SEQ ID NO 8561
LENGTH: 921
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Bublication No. US2005027917A1

GENERAL INFORMATION:

FULL OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 2300-21302

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: US/10/779,555

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR APPLICATION NUMBER: 00/06,555

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-12

PRIOR FILING DATE: 1998-10-12

PRIOR FILING DATE: 1998-10-12

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-01-28

PRIOR PRIOR
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Remaining Prior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.1;
0; Mismatches 33;
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APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: APATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
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61.2%;
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HORIKAWA, HIROSHI
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Matches 52; Conservative
OMURA, SATOSHI
IKEDA, HARUO
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APPLICANT:
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DEROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOO73
CURRENT APPLICATION NUMBER: 06/15/,832
PRIOR PELING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR PELING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASEUSE for Windows Version 4.0
LENGTH: 1342
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Sequence 38434, Application US/11097143
Eublication No. US200502085S8A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
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                                                                                                       717 GTTGGCCACATGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 762
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                                                           77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                 Sequence 38495, Application US/11097143 Ublication No. US20050208558A1 GENERAL INFORMATION: APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.7
Matches 59; Conservative
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                                                                                                         October 24, 2005, 18:41:53 ; Search time 60.1934 Seconds (without alignments) 4811.505 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-902-540-2371
US-09-902-540-1101
US-09-252-991A-12370
US-09-252-991A-12333
US-09-252-991A-12333
US-09-126-121-22
US-08-126-121-22
US-08-126-121-22
US-09-126-121-22
US-09-126-121-22
US-09-126-121-23
US-09-902-540-1213
US-09-902-540-1213
US-09-949-016-13193
US-09-949-016-13134
US-09-949-016-13134
US-09-949-016-13134
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Maximum Match 100%
Listing first 45 summaries
                                                                          - nucleic search, using sw model
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Match Length DB
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Maximum DB
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US-09-252-991A-12692/C

US-09-252-991A-12692/C

Sequence 12692, Application US/09252991A

Sequence 12692, Application US/09252991A

Patent No. 6551795

GRERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINGA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINGA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12692
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                  Sequence 5551, Ap Sequence 5551, Ap Sequence 5035, Ap Sequence 3318, Ap Sequence 1110, Ap Sequence 1154, Ap Sequence 1154, Ap Sequence 200, App Sequence 21, Appli Sequence 21, Appli Sequence 219, App Sequence 219, App
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17417, A
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Patent No. 683347
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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US-09-252-991A-14970
US-09-902-540-2474
US-09-902-540-2059
US-09-902-540-2059
US-09-902-540-3118
US-09-902-540-118
US-09-902-540-110
US-09-902-540-110
US-09-902-540-1154
US-09-902-540-1154
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US-09-902-540-1154
US-09-902-540-1154
US-09-252-991A-193
US-09-252-991A-193
US-09-252-991A-219
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US-09-949-016-17417
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) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12370
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; ORGANISM: Pseudo
US-09-252-991A-12323
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(1584)B
CURRENT APPLICATION NUMBER: 103/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1101
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Pred. No. 4.3;
0; Mismatches 47; Indels 0;
                                                                                                                                                                   Score 29.8; DB 4; Length 1311;
Pred. No. 2.1;
0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                  105 TGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                428 GGAACGGGÁCATTGGÁCGCCCGCCGGTCACGCTCTTTACCCCCA 472
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Sequence 12370, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1101, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                                Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-1101
                                                                  TYPE: DNA ORGANISM: Myxococcus xanthus
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SEQ ID NO 12370
LENGTH: 585
NUMBER OF SEQ ID NOS: 16825
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                                                                                                                     US-09-902-540-2371
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                 SEQ ID NO 2371
LENGTH: 1311
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MacC 3. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12097
LENGTH: 1443
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                                                                                                                                8 CGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGA
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   DB 4; Length 585;
                                                                  Indels
Query Match
16.2%; Score 28.6; D
Best Local Similarity 53.0%; Pred. No. 4.3;
Matches 61; Conservative 0; Mismatches
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; Sequence 12233, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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55 ACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGCTTATCTCTCATGCGCGTGAC 114
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Fatent No. 6522051
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 2091;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wilpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE:
CLASSIFICATION:
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16.2%; Score 28.6; DE
Best Local Similarity 58.0%; Pred. No. 6.3;
Matches 69; Conservative 0; Mismatches
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NAME/KEY: Human NRG3B2 (hNRGB2)
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: COALGY, Delicate L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P108:
TELECHONE: 650/252-2066
TELECHONE: 650/252-2066
TELERAX: 650/252-981
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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NAME: COALGY, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P108
TELEPHONE: 650/255-2066
TELEPHONE: 650/255-2066
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INFORMATION FOR SEQ ID NO: 22:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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| IDENTIFICATION METHOD:
| OTHER INFORMATION:
US-08-899-437-22
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TOPOLOGY: Linear
FEATURE:
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Sequence 12237, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12237

LENGTH: 2085
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Patent No. 6121415

CENERAL INFORMATION:
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CENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
CORRESPONDENCE ADDRESS:
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STREET:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
CORRESPONDENCE ADDRESS:
CITY:
CORRESPONDENCE ADDRESS:
STREET:
CALLED ADDRESSEE:
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                                                              DB 4; Length 1551;
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Best Local Similarity 53.0%; Pred. No. 6.3;
Matches 61; Conservative 0; Mismatches 54; Indels
                                                         Query Match 16.2%; Score 28.6; DB 4; Length 1!
Best Local Similarity 53.0%; Pred. No. 5.8;
Matches 61; Conservative 0; Mismatches 54; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: PLAN PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jul-1997
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12237
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US-09-252-991A-12237
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55 ACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGAC 114
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Sequence 123, Application US/09902540
Patent No. 683347
Patent No. 683347
Patent No. 683347
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Seven C.
APPLICANT: Was a seven C.
APPLICANT: Was and Uses Thereof FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT:
APPLICANT:
GENERAL INFORMATION:
APPLICANT:
GOGOWSKi, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION:
Ligands and Uses Therefor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STRATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28.6; DB 3; Length 2502;
Pred. No. 6.7;
0; Mismatches 49; Indels 1
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| LOCATION: 1-2502
| IDENTIFICATION METHOD: OTHER INFORMATION: US-09-126-121-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P1084R1D1
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NAME: CON16Y, Deitche L.
REGISTRATION NUMBER: 36,487
REFRENCE/DOCKET NUMBER: P108.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-2066
TELEPAX: 650/952-9881
                                                                                                                                        US-09-126-121-5
; Sequence 5, Application US/09126121
; Patent No. 6252051
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Best Local Similarity 58.0%;
Matches 69; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2502 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT to Application US/08899437; Sequence 5, Application US/08899437; Sequence 5, Application US/08899437; Sequence 5, Application US/08899437; Sequence 10. 6121415; Patent No. 6121415; Turb No. 6121415; Turb OF INVENTION: ExbB Receptor-Specific Neuregulin Related; TITLE OF INVENTION: Ligands and Uses Therefor; TITLE OF INVENTION: Ligands and Uses Therefor; NUMBER OF SEQUENCES: 23; CORRESPONDENCE ADDRESS: ADDRESSE: Generatech, Inc. ADDRESSE: Generatech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                             1;
                                                                                                                                                                Query Match 16.2%; Score 28.6; DB 3; Length 2091; Best Local Similarity 58.0%; Pred. No. 6.3; Matches 69; Conservative 0; Mismatches 49; Indels 1
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16.2%; Score 28.6; DB 3; Length 2502;
Best Local Similarity 58.0%; Pred. No. 6.7;
Matches 69; Conservative 0; Mismatches 49; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,487
BER: P1084R1
Human NRG3B2 (hNRGB2)
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NAME: CONLey, Deirdre L.
REGISTRATION NUMBER: 36,487
REPERENCE/DOCKET NUMBER: 108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-2066
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TYPE: Nucleic Acid
STRANDEDNESS: Single
                       LOCATION: 1-2091
DENTIFICATION METHOD:
CTHER INFORMATION:
US-09-126-121-22
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) IDENTIFICATION METHOD:
) OTHER INFORMATION:
US-08-899-437-5
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RESULT 14
JS-09-513-999C-27806
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 13983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TTATCGTGACAGGACGCCAGCTTCCTGTGCTAACCGCAGCCGGACGCAACTCCTTAT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.6; DB 4; Length 25048;
Pred. No. 13;
0; Mismatches 79; Indels 0;
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16.0%; Score 28.4; D
Best Local Similarity 49.3%; Pred. No. 20;
Matches 74; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/902,540
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US-09-949-016-113983/c
; Sequence 13983, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
                                      CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1239
LENGTH: 25048
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Myxococcus xanthus
US-09-902-540-1239
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Best Local Similarity 49.04
Matches 76; Conservative
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ORGANISM: Human
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          GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATEL NO. 6783961
FILE REPERBUCE: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR PAPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 27806
LENGTH: 283
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinfle, Gregory J.
APPLICANT: Hinfle, Gregory J.
APPLICANT: Hinfle, Gregory J.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxcoccus xanthus Genome Sequences and Uses Thereof FILE BERERNCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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15.9%; Score 28.2; DB 4; Length 285
Best Local Similarity 54.3%; Pred. No. 9.6;
Matches 57; Conservative 0; Mismatches 48; Indels
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Pred. No. 4.8;
Sequence 27806, Application US/09513999C
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10-09-902-540-7217

1 Sequence 7217, Application US/09902540

1 Patent No. 6933447
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US-09-513-999C-27806
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Best Local Similarity 68.4%;
Matches 39; Conservative
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LOCATION: 196
OTHER INFORMATION: m=a
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LOCATION: 197
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LOCATION: 198
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- 1657 CAGGTGACGGCTTCGCGGGTTGCTCGCTCCAGCCCAACGCCGGAAGCCAGGGGAGTAC 1716 g & g

Search completed: October 24, 2005, 21:57:49 Job time : 63.1934 secs

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192483 Sequence 1
103664 Sequence 2
G02286 human STS S
CQ513678 Sequence
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M12465 Bacteriopha
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AR038286 Sequence
AR075283 Sequence
AR152695 Sequence
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AX323349 Sequence
CQ504346 Sequence
AX361570 Sequence
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BD175852 A method
AX404725 Sequence
CQ504404 Sequence
CQ513399 Sequence
E00523 Double-stra
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AJ535749 Cicer ari
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161307 Sequence 11
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Grigliatti, T.A., Theilmann, D.A., Pfeifer, T.A. and Hegedus, D.D. Insect expression vectors Pacent: JP 200151625-A 13 25-SEP-2001;
THE UNIVERSITY OF BRITISH COLUMBIA
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PN JP 2001516225-A/13
PD 25-SEP-2001
PF 26-MAR-1998 JP 1998541010
PR 27-MAR-1997 US 60/049946,28-JAN-1998 CA
THOMAS A GRIGILATTI, DAVE A THELMANN, THOWAS
A PFEIFER, DWAYNE D
PI HEGEBUS
PC INSECT expression vectors
CC Insect expression vectors
FH Key
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    .50
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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CQ504346
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Matches 50; Conservative
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
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AC013324 Homo sapi
AC013315 Homo sapi
AC015852 Homo sapi
AC015862 Homo sapi
AC073998 Homo sapi
G39061 Z11905 Zebr
BD268301 33 human
G40613 Z7956 Zebra
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CQ406071 Sequence
AC02384 Homo sapi
AC016798 Homo sapi
AC016095 Homo sapi
AR006095 Homo sapi
AR022751 Sequence
AR359133 Sequence
                                                                                                    October 24, 2005, 18:40:53 ; Search time 302.908 Seconds (without alignments) 7998.346 Million cell updates/sec
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Compugen Ltd.
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Copyright (c) 1993 - 2005
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Listing first 45 summaries
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Gaps

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Result 8

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contig of 727 bp.
659; gap of 100 bp.
63: contig of 804 bp.in.
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3: gap of 100 bp.
670; bp.in.
670; pp. of 777 bp.in.
770; pp.in.
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 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckelly, R., Boquelavkty, L., Boukhgalter, B., Bown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreita, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardynas, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Morkenan, K., McLaughlin, J., Melfrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Sancos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                             ACULJ392 99591 bp DNA linear HTG 13-JUL-2000 HOMO sapiens chromosome 2 clone RP11-429N24 map 2, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (109-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6425709.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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* sequencing reads that have not been assembled into

* contigg. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.
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contig of 799 bp in length
contig of 799 bp in length
gap of 100 bp
contig of 809 bp in length
gap of 100 bp
contig of 812 bp in length
gap of 100 bp
contig of 777 bp in length
gap of 100 bp
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g of 779 bp in length
f 100 bp
g of 768 bp in length
                                                                                                                                                                                           (bases 1 to 99591)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
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gap of 100
contig of
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                                                                                                                    AC013392.3 GI:9123920
HTG; HTGS_PHASE0.
Homo sapiens (human)
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JOURNAL
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COMMENT

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2 Chases 1 to 11822)

Bildwin, J., Barra, N., Backerly, R., Baguslavkiy, L., Boukhgalter, B., Baldwin, J., Barra, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barra, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Backerly, R., Collins, S., Collymore, A., Devarellano, K., Devar, C., Runk, R., Gage, D., Gaddyan, J., Gardyna, S., Grart, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Uohnson, R., Morkernan, K., McCanold, P., Marquis, N., McEwan, P., McCark, A., Mokcertan, K., McLaughlin, J., Marquis, N., McEwan, P., McCark, A., Mokcertan, K., McLaughlin, J., Marquis, N., McEwan, P., McCark, A., Mokcertan, K., McCanon, T., O'Donnell, P., Stange-Thoman, N., Stolyman, C.H., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasillav, H., Noy, A., Santos, R., Severy, P., Stange-Thoman, N., Stolyman, C.H., Warm, D., Yew, W., J., Zimmer, A. and Zody, M., Subramanian, A., Talamas, J., Warm, D., Yew, W., J., Zimmer, A. and Zody, M., Golleler, J., Boukhgalter, B., Strom, A., Badds, E., Baddyni, J., Barna, N., Bastran, V., Beda, E., Lincon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastran, V., Beda, E., Lincon, L., Musbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastran, V., Beda, E., Collymore, A., Castel, A., Choepel, Y., Colanger, M., Colange, D., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Raritas, A., Klein, J., Laskoque, K., Lamazares, B., Haftock, A., McCark, M., Santos, R., Schace, E., B., Goyette, M., Collara, V., Raymond, C., Rile, C., Liu, G., Loucke, K., McCark, M., McCark, M.,
                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 22, clone RP11-348B6
                   AC013315.3 GI:9123904
HTG; HTGS PHASE0.
Homo sapiens (human)
                                                                                                              (bases 1 to 118229)
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                                                                  Homo sapiens
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                    VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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J of 781 LE
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c of 765 bp in length
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g of 754 bp in length
f 100 bp
g of 822 bp in length
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g of 837 bp in length
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Best Local 9
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* NOTE: This record contains 124 individual

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows

ACU13315 Homo sapiens chromosome 22 clone RP11-348B6 map 22, LOW-PASS SEQUENCE SAMPLING.

RESULT 3 AC013315 LOCUS DEFINITION

3876 Traarrecerececereacrecececerriceaerecesaaacereres

Center project name: L3764 Center clone name: 348_B_6

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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                  contig of 765 bp in length gap of 100 bp contig of 801 bp in length contig of 801 bp in length gap of 100 bp contig of 842 bp in length gap of 100 bp contig of 822 bp in length gap of 100 bp contig of 822 bp in length gap of 100 bp contig of 764 bp in length gap of 100 bp contig of 764 bp in length gap of 100 bp contig of 764 bp in length
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		otion of the control	11967 bp DNA linear HTG 13-JUL-2000 -11016, LOW-PASS SEQUENCE SAMPLING. -1016, CMPLEBERTER, Exteleostomi, -10167 Craniata, Vertebrata, Euteleostomi, -10168 Catarrhini, Hominidae, Homo.
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100 bp
of 658 bp in length
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Saldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castlef, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McDewan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., McDewan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Morrow, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McTow, J., Lieu, C., Locke, K., McGonald, P., Marquis, N., Stonge-Thomann, N., Stoojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassliev, H., Vo, A., Wheeler, J., Wu, X., Wwman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 19, 2000 this sequence version replaced gi:8099785.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/Repeatmasker.html
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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      Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-11016
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COMMENT

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4832:
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone CTB-155C15
Upublished
Upublished
Series 1 to 260636)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC015852 260636 bp DNA linear HTG 24-AUG-2002
Homo sapiens chromosome 18 clone CTB-155C15 map 18, LOW-PASS
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contig of 655 bp in length
gap of 100 bp
gap of 100 bp
gap of 100 bp
contig of 643 bp in length
gap of 100 bp
contig of 670 bp in length
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g of 645 bp in length
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contig of 668 bp in length
gap of 100 bp
contig of 637 bp in length
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of 672 bp in length
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of 742 bp in length
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of 670 bp in length
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of 647 bp in length
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           bp in length
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Pred. No. 0.0032;
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gap of 100
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54250: gap of 1
54986: contig c
            contig c
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85.4%;
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Brown A., Castle A., Colangelo, W., Collins, S., Collymore, A.,
Galagna, J., Castplan, S., Grent, G., Hagos, B., Hadrod, A., Hotton, J.,
Galagna, J., Castplan, S., Grent, G., Hagos, B., Hadrod, A., Hotton, J.,
Ichack, J., Lisu, C., Locke, K., Macdonald, P., Martus, M.,
McDann, P., McChrit, A., Werkernan, K., Katales, A., Kiein, J.,
Merzon, C., Moure, A., Werkernan, K., Katales, M., Kiein, J.,
Merzon, C., Naylor, J., Morran, C.H., O'Connor, T., O'Donnell, P.,
Brange-Thoman, R., Lisu, C., Locke, K., Macdonald, P., Martus, M.,
Martin, B., Martin, B., Martin, J., Maltin, J., Maltin, J.,
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Martin, B., Martin, B., Martin, M., Wasalister, M., Wasalister, M., Wasalister, J., Whateler, J., Wh. X.,
Martin, J., Lincon, L., Nusbaun, C., Lander, E., Abraham, H., Allen, N.,
Martin, M., Martin, M., Martin, M., Martin, M., Martin, J.,
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0: gap of 100 bp
2: contig of 872 bp in length
3: gap of 100 bp
1: contig of 882 bp in length
3: gap of 100 bp
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contig of 877 bp in length
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contig of 886 bp in length
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5: contig of 880 bp in length
6: gap of 100 bp
7: contig of 887 bp in length
7: gap of 100 bp
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7: contig of 875 bp in length

7: gap of 100 bp

5: contig of 867 bp in length

6: gap of 100 bp
gap of 100 bp
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of 890 bp in length
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contig of 876 bp in length
gap of 100 bp
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of 885 bp
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ACC10800 73282 bp DNA linear HTG 23-SEP-1999
Homo sapiens clone 1_E_17, LOW-PASS SEQUENCE SAMPLING.
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(bases 1 to 73282)

Birran, B. Linton, N., Nackerly, R., Boguslavkiy, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karates, A., Klein, J.,

McEwan, P., McCkernan, K., Macdonald, P., Marquis, N.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Edwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 73282)

Birran, B. Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone 1_E_17
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Homo sapiens clone RP11-337M23, LOW-PASS SEQUENCE SAMPLING.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-337M23
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В

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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wiman, D., Ye, W. J., Direct Submission

L. Submitted (199-JUL-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
ON Sep 30, 2000 this sequence version replaced gi:9818018.
All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: 1.7934
Center clone name: 337_M_23
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G39061 Cabrafish AB Danio rerio STS genomic, sequence tagged site. G39061. G1:3358270
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( Cypriniformes; Cyprinidae; Danio.

I ( bases I to 604)

Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E., Kaplan, S., Jackson, D., de Sauvage, F., Jacob, H. and Fishman, M.C.

Zebrafish genetic map with 2000 microsatellite markers

Genomics 58 (3), 219-232 (1999)

10373319
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Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishmandmgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: CACCGAGCTTCACTCAGACGTA
Primer B: ATACACACCCAAGCCGACAT
STS size: 112
PCR Profile:
PRESOak: 94 degrees C for 5.0 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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94 degrees C for 1.0 m:
58 degrees C for 1.0 m:
27 degrees C for 1.5 m:
27 mJ Research PTC-100
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Pred. No. 0.0054;
0; Mismatches
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of 662 bp i
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of 690 bp
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of 675 bp
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Best Local Similarity 83.7%;
Matches 41; Conservative
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PCR Cycles: 2
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AUTHORS
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C12021/02, C1201/02, C1201/03, C1201/02, C1201
        A61P1/16, A61P3/10, A61P5/00, A61P7/02, A61P7/04, A61P7/06, A61P7/08, PC
                                                                                                            AGIPIL/06, AGIPI3/02, AGIPI3/03, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 826)
Shimoda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S., Zackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.
Zebrafish genetic map with 2000 microsatellite markers
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Z7956 Zebrafish AB Danio merio STS genomic, sequence tagged site.
G40613
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Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Pax: 6177265806
                                                                                    A61P9/06, A61P9/08, A61P9/10, A61P9/12, A61P9/14, A61P11/00
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http://zebrafish.mgh.harvard.edu
Primer A: CACATGTGCACCGGACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .745
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OS HOMO Sapiens (human)
PN 22-0CT-2002
PF 18-12A-2000 UP 200594904
PR 19-12AN-1999 US 60/116330
PR 19-12AN-1999 US CALIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PI PAUL A MOORE, GEORGE KOMATSOULIS, CHARLES E BIRSE PC CL2N15/09, A61K31/7115, A61K35/76, A61K38/00, A61K45/00, A61K48/00, PC PC PC PC
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Rosen, C.A., Ruben, S.M., Ebner, R., Young, P.E., Ni, J., Moore, P.A., Rometsoulis, G. and Birse, C.B.
33 human secreted proteins
Patent: JP 2002534972-A 36 22-OCT-2002,
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                                                                                                                                                                                                                                                                                                                                                                                       Primers are available from Research Genetics Inc.
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Location/Qualifiers
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dNTPs: each 200 uM
Tag Polymerase: 0.034 units/ul
Total Vol: 10 ul
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/dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
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/mol_type="genomic DNA"
/strain="AB"
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'sex="F"
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JP 2002534972-A/36.
Homo sapiens (human)
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KCl:
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STS 01-FEB-2001

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/Glone lib="Zebrafish AB"
/dev stage="Adult"
/lab_host="DH5alphaF'IQ"
/lab_host="DH5alphaF'IQ"
/note="Vectors: mi3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with Alul, Cac81, HaeIII, NlaVI, or
RsaI. Fragments in the range of 250-500 bp were gel
purified and a BstXI linker was added. The fragments were
cloned into a modified Mi3mp19 vector and transformed
into B. COli DH5alpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                                                 Cardiovascular Research Center
Massachusetts General Hospital
Mall code 194100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Bmail: fishmandmgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
primer A: TCAATCTGTCAAACTCCGCA
Primer B: CGCTTTATAGGGCTGCAGAG
STS size: 244
PCR Profile:
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Zebrafish genetic map with 2000 microsatellite markers Genomics 58 (3), 219-232 (1999) 99303552
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                                                                                                                                                                                                                                                                                                                    94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute 27
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Location/Qualifiers
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50 mM
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/mol_type="genomic DNA"
/strain="AB"
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120. .139
complement(344. .363)
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/map="LG 16"
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                                                                                                     Contact: Mark C. Fishman
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Thermal Cycler:
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Taq Polymerase:
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Polymerization:
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/dev stage="Adult"
/lab_host="DHSalphaF'IQ"
/lab_host="DHSalphaF'IQ"
/note="Vector: mi3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with Alul, Cac81, HaeIII, NIAVI, or
Rsal. Fragments in the range of 250-500 bp were gel
purified and a BstXI linker was added. The fragments were
cloned into a modified Mi3mp19 vector and transformed
into E. Coli DHSalpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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1 (Jases I to 979)
Shimoda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S., Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.
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Pred. No. 0.0068;
0; Mismatches 8; Indels 0
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94 degrees C for 1.0 minute
58 degrees C for 1.0 minute
72 degrees C for 1.5 minute
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5 mM
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Thermal Cycler: MJ Research PTC-100
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each 200 uM
0.034 units/ul
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/mol_type="genomic DNA"
/strain="AB"
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/map="LG 16"
Primer B: TCTCTCCCCTGGACATCATC
STS size: 142
PCR Profile:
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complement(187. .206)
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Tris-HCl:
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Danio rerio
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1 Similarity 83.3%;
40; Conservative (
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G40162.1 GI:3359371
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Annealing:
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All repeats were identified using Repeatmasker:
Smit, A. F. A. R. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/Repeatmasker:html
                       HTG 13-JUL-2000
                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo. (base 1 to 76295)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens chromosome 15, clone RP11-165921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....-Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
ACULIS42 13-JUN HOMO SADIENCE SAMPLING. SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This record contains 86 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
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888: gap of 100 bp

1671: contig of 783 bp in length

1771: gap of 100 bp

2563: contig of 792 bp in length

2663: gap of 100 bp

3454: contig of 791 bp in length

4331: contig of 777 bp in length

4431: gap of 100 bp
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Center clone name: 165_P_21
                                                                                                                             AC023542.2 GI:9156023
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Homo sapiens (human)
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Gaps

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Birren, B., initon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Erowh, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colanger, K., Dodge, S., Collymore, A., Cooke, P., DeArellano, K., Deward, S., Collymore, A., Cooke, P., DeArellano, K., Deward, S., Collymore, A., Cooke, P., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, P., Fitzhugh, W., Forrest, C., Gage, D., Grand, P., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Johes, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., McEwan, E., Milrova, T., Macdonald, P., Marquis, N., McCarthy, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Medrim, J., Norrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Severy, P., Spencer, B. Stande, T., Roy, A., Santos, R., Schauer, S., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Direct, Bobmission
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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AC02384.2 GI:9144035
HTG; HTGS PHASE0.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC023384 75002 bp DNA linear HTG 13-JUI
Homo sapiens chromosome 11 clone RP11-589112 map 11, LOW-PASS
SEQUENCE SAMPLING.
                                                                       Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: W O 170979-A 13142 27-SEP-2001,
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. 586
| organism="Homo sapiens"
| mol type="unassigned DNA"
| /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    516 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAACCTGTCG 565
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                                                                                                                                                                                                                                                                                     Query Match 71.2%; Score 35.6; DB 6; Length 586; Best Local Similarity 82.0%; Pred. No. 0.008; Matches 41; Conservative 0; Mismatches 9; Indels
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-589112
Unpublished
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                                                         Lee, J. and Lillie, J.
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Pred, No. 0.0076;
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y of 759 bp in length

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q of 767 bp in length
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CQ406071
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Query Match Best Local 8

Matches

DEFINITION ACCESSION

VERSION

RESULT 13 CQ406071

LOCUS

KEYWORDS SOURCE ORGANISM

* NOTE: This record contains 88 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved. 54: contig of 746 bp in length
4: gap of 100 bp
8: contig of 764 bp in length
9: contig of 764 bp in length
1: gap of 100 bc contig of 724 bp in length gap of 100 bp contig of 749 bp in length gap of 100 bp contig of 773 bp in length gap of 100 bp contig of 773 bp in length gap of 100 bp contig of 773 bp in length gap of 100 bp contig of 743 bp in length gap of 100 bp contig of 743 bp in length gap of 100 bp contig of 743 bp in length gap of 100 bp contig of 743 bp in length gap of 100 bp contig of 743 bp in length gap of 100 bp gap of 100 bp gap of 100 bp contig of 751 bp in length gap of 100 bp contig of 754 bp in length gap of 100 bp 9 00 764 bp in length f 100 bp f 100 bp g of 760 bp in length g of 760 bp in length f 100 bp f 100 bp in length f 100 bp g of 762 bp in length g of 741 bp in length 100 bp 10 100 bp 100 ft 100 pp 10 f 100 bp g of 754 bp in length f 100 bp g of 748 bp in length 761 bp in length 100 bp of 783 bp in length in length 100 bp contig gap of contig gap of contig c gap of 1 contig c contig gap of 724. 1824. 1824. 1673. 1328. 1 11950: 13653: 14392: 5244: 18615: 18715: 21205: 21305: 22089: 22189: 22972: 11078: .6095: .6927: 2812: 3553: 4492: 6195: 7027: 1766: 7866: 9489: 9589: 2456 33556 33556 44180 4 14493 15245 15345 16096 16196 16928 17028 17767 17867 18616 18716 19490 19590 20445 21206 21306 22090 22190 22190 23073 23827 23927

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L. Submitted (07-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6532117.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU16/98 95127 bp DNA linear HTG 13-JUL-2000
Homo sapiens clone RP11-1J15, LOW-PASS SEQUENCE SAMPLING.
AC016798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
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                                                                                                                                                                                                                       Score 35.6; DB 2; Length 75002;
Pred. No. 0.009;
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contig of 772 bp in length
gap of 100 bp
contig of 721 bp in length
gap of 100 bp
contig of 744 bp in length
gap of 100 bp
contig of 748 bp in length
contig of 748 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1J15
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Web site: http://www-seq.wi.mit.edu
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HTG; HTGS PHASE0.
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82.0%;
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Gaps 20592 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGAAACCTGTCG 20641 ö 20 Length 95127; 1 ACTIMAGCTIANAGGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 9; Indels Query Match 71.2%; Score 35.6; DB 2; Best Local Similarity 82.0%; Pred. No. 0.0091; Matches 41; Conservative 0; Mismatches 9; ò

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Search completed: October 24, 2005, 20:18:17 Job time : 311.908 secs

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CNSO7H0H
Anopheles gambiae GSS T7 end of clone 23P13 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
                                        BQ907999 Q002002 O
BM419897 R020C12 O
CB865576 H1010A15w
AGG0720 Pan trog1
AG13113 Pan trog1
AG114861 Pan trog1
AG17143 Arabidops
CF569104 79325 5'U
B1937595 dd94b01.y
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Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                          B30742 HS-1003-A1-
BF703023 MI-P-E5-a
                                                                                                                                            AG109195 Pan trogl
AG045821 Pan trogl
CL096240 ISB1-27L3
                                                                                                                                                                       AQ041632 CIT-HSP-2
CC961712 BOIDY76TF
                AU069599
BP874955
BJ671717
                                                                                                                                                                                                                                                                                                                                                                                                            Web: www.genoscope.cns.fr)

2 (bases 1 to 412)

Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.

Direct Submission
Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea;
                 AU069599 A
BP874955 B
BJ671717 B
BQ907999 C
BM419897 R
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Anopheles gambiae
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Pred. No. 0.00023;
0; Mismatches 6;
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                                                                                                ATH517143
CF569104
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CL096240
AQ041632
                                   BJ671717
BQ907999
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AG060720
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BP874955
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BF703023
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AL610451.1 GI:15916636
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Best Local Similarity 87.5%;
Matches 42; Conservative 0
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1 (bases 1 to 412)
Genoscope.
DEFINITION
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UMC-p8mm2
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AQ076128 C
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ALC10727
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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/organism="Homo sapiens"
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Homo sapiens
Map Building
Unpublished (1998)
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                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 125)
S Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                     AQ080570 125 bp DNA linear GSS 20-AUG-1998
CIT-HSP-2358MZ.TF CIT-HSP Homo sapiens genomic clone 2358M2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 20-AUG-1998
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3.21
Class: BAC ends.
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1 (Dases 1 to 174)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, B., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC Bnd Sequence Database for Sequence-Ready
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Pred. No. 0.00082;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2358M2"
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                                                                                                    genomic survey sequence
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GSS.
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1 Similarity 85.4%;
41; Conservative (
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Homo sapiens
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Best Local Similarity
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COMMENT
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AUTHORS
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                              RESULT 2
AQ080570
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AQ076128
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
710 Institute for Genomic Research
711 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Featl: mddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiner, variety of a random human BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tel: 301 B38 0208
Fax: 301 B38 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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1 (bases 1 to 177)

Adams, N.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3-21
Class: BAC ends.
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Seg primer: Ml3-21
Class: BAC ends.
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41;

Matches

DEFINITION

RESULT 5 AQ076114 ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

Query Match

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http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures
discussed in this section have been described in detail
elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
Jiang et al., 2001). Total cellular RNA from each sample
was isolated by using STAT-60 reagent (Tel-Test,
Friendswood, TX) and poly(A) + RNA was obtained by two
rounds of purification with the Oligotex mRNA isolation
kit (Qiagen) according to the manufacturer's instructions.
The oviduct libraries and the Day 3, 6 and 10 endometrium
libraries were constructed essentially as described by the
manufacturer's instructions provided with the SuperScript
Plasmid System (Invitrogen, cat. no. 18248-013). Briefly,
Img of poly(A) + RNA will be annealed at 37 degrees Celsius
with 10mg of NotI-tag-dT18 oligonucleotide
(GCTGCTGCGCCCC-tag-T18) and reverse transcribed at 37
degrees Celsius with SuperScript II (Invitrogen) reverse
transcriptase (Jiang et al., 2001). The 'tag' represents at
fissue/stage-specific ten-base sequence identifier
(http://genome.uiowa.edu/pubsoft/software.html) present in
the oligonucleotide used to prine first-strand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis and digested directionation
columns (Invitrogen-Life technologies). The cDNAs derived
from and developmental stage of a particular tissue were
mixed on an equimolar basis and ligated directionally into
the NotI and Sall sites of the DSPORTI vector
                                                                                                                                                                                     Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Dases 1 to 372)
S Kim,J., Whitworth,K.M., Springer,G.K., Bivens,N.J., Ries,J.E.,
Woods,R.J. Spollen,W.G., Forrester,L.J., Mathialagan,N.,
Prather,R.S. and Green,J.A.
Large-scale Generation and Analysis of Expressed Sequence Tags from
Porcine endometrium and oviduct
Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia, MO 65212, USA
Tel: (573)882-0428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Company to the University of Missouri. Genetic Source:
Company to the University of Missouri. Genetic Source:
Company to the University of Missouri. Genetic Source:
Endometrium and oviduct tissues from various stages of the
estrous cycle were collected from crossbred pigs (Sus
scrofa domestica), frozen in liquid nitrogen immediately
after collection, and stoored at -80 degrees Celsius until
RNA extraction. The specific tissues collected were Day 0
and Day 3 whole oviducts and Days 3, 6, 10 and 12-14
endometrium. More information regarding the methods can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev stage="Oviduct from a gilt on day 3 of the estrous cycle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
scrofa cDNA 3', mRNA sequence.
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                                                       CO990192.1 GI:51349466
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CIT-HSP-2368K7.TF CIT-HSP Homo sapiens genomic clone 2368K7,
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Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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UMC-pd3ov2-002-g02 Oviduct gilt D3 of estrous cycle pd3ov Sus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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                    /cell_rype="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (cell type="Sperm"
clone lib="CIT-HSP"
note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                           73.6%; Score 36.8; DB 8; Length 177; llarity 85.4%; Pred. No. 0.00086; Conservative 0; Mismatches 7; Indels (
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'db_xref="taxon:9606"
'clone="2368K7"
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Homo sapiens
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Best Local Similarity 85.4
Matches 41; Conservative
                                                                                                                             HindIII"
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Class: BAC ends.
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RESULT 6 CO990192 LOCUS DEFINITION

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Jiang, H., Whitworth, K.M., Bivens, N.J., Ries, J.E., Woods, R.J., Forrester, L.J., Springer, G.K., Mathialagan, N., Agca, C., Prather, R.S. and Lucy, M.C. Large-scale Generation and Analysis of Expressed Sequence Tags from
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine Ovary
Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
Mol6 Medical Sciences Bldg., Columbia, MO 65212, USA
Fax: (573)884-5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: porcine@rnet.missouri.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                    C0947892.1 GI:51314651
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                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (pig)
Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
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CO947892
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Location/Qualifiers

FEATURES

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Activity man "8us serrofa",

Adu Yrefa" taxon: 992,"

Adu Yrefa" taxon: 992,"

Adu Yrefa" taxon: 992,"

Adu Engelan was over the follicle",

Actor in the property Funding: A grant from the Monsanto

Company to the University of Missouri, Ganetic Source:

Ovarian tissue (whole overy, dissected follicles, or

corpora lutes) was collected from crossbred pigs 61ss

scrofd domestica), frozen in liquid nitrogen shortly after

collection, and stored at 90 degrees collsis until RNA

extraction. The tissue from several individual pigs was

spooled for the purpose of RNA extraction. The specific

tissues collected were fetal whole ovary; neonatal whole

covary; prepubutal whole ovary; a 4,6 and 8 mm growing

follicles; bay 0 follicles; bay; Samil antral follicles

and ocropora lutes aby 12 corpora lutes and pay 12

found at:

http://denome.rnet.missouri.edu/Swine/Methods.html.

http://denome.rnet.missouri.edu/Swine/Methods.html.

http://denome.rnet.missouri.edu/Swine/Methods.html.

http://denome.rnet.missouri.edu/Swine/Methods.html.

https://denome.rnet.missouri.edu/Swine/Methods.html.

https://denome.rnet.missouri.edu/M
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/de_rist__cantinger;
/de_rist__cantinger;
/de_rist__cantinger;
/clone_lib="pnatal"
/clone_lib="pnatal"
/clone_lib="pnatal"
/note="vector: pSport!; Funding: A grant from the Monsanto
Company to the University of Missouri. Genetic Source:
Company to the University of Missouri. Genetic Source:
Company to the University of Missouri. Genetic Source:
Corpora_lutea) was collected from crossbred pigs (Sus
corpora_lutea) was collected from crossbred pigs (Sus
scrofa domestica), frozen in liquid nitrogen shortly after
collection, and stored at -80 degrees Celsius until RNA
extraction. The tissue from several individual pigs was
pooled for the purpose of RNA extraction. The specific
tissues collected were fetal whole overy; neonatal whole
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1 (Dases 1 to 425)
Jiang, H., Whitworth, K.M., Bivens, N.J., Ries, J.E., Woods, R.J., Forrester, J., Springer, G.K., Mathialagan, N., Agca, C., Prather, R.S. and Lucy, M.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO954011 425 bp mRNA linear EST 09-SEP-2004 UMC-pnatal4-004-e04 Perinatal ovary pnatal Sus scrofa cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea and Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Blotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA ThG TISSUE-8Mm ovarian follicle
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Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Contact: DNA Core Facility (Swine Project)
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, M0 65212, USA
Tel: (573)882-0428
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Email: porcine@rnet.missouri.edu
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/organism="Sus scrofa"
/mol_type="mRNA"
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ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 CO954011

LOCUS

REFERENCE AUTHORS

TITLE

FEATURES

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Sequence loantlier

(http://genome.ulowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to Sall adapters (Invitrogen-Life echnologies) and digested with NoLI. The CDNAs will be size selected by passage through CDNA size fractionation columns (Invitrogen-Life technologies). The CDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NoLI and Sall sites of the pSPORTI vector.

(Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polya+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%) etc.) and to provide a sequence database clones were sequenced at the University of Missouri-Columbia DNA Core Facility Bioinformatics work was performed by GK Springer's bloinformatics group (%5 Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clones Requestes; Requests for clones
Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, Immy of poly(A)+ RNA will be annealed at 37 degrees (GETCCTGGGGCGCG-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcribteds at state transcriptese (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Should be made to the Director of the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res. 1996; 6:791-806.

2. Jiang H, Bivens NJ, Ries JE, Whittworth KM, Green JA, Forrester LD, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly (dA) tails.
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Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
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TAG_TISSUE=Perinatal ovary
TAG_SEQ=Not found"
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ORIGIN

Gaps ô DB 7; Length 425; 73.6%; Score 36.8; DB 7; Length 42: 85.4%; Pred. No. 0.001; live 0; Mismatches 7; Indels 41; Conservative Query Match Best Local Similarity Matches 41; Conserv

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RESULT 9 BE403103 LOCUS

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BE403103

mRNA 451 bp

linear

EST 21-JUL-2000

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                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooideae; Triticae; Triticae.

1 (bases Triticae; Triticae.

2 (bases Triticae.

3 Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,

Gloutier,P., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,

Joudrier,P., Harmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,

Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,

Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,

Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

Unpublished (2000)

Contact: Jacquemin JM

Centre de Recherches Agronomiques, Departement de Biotechnologie

23 chaussee de Charleroi, 5030 Gembloux BELGIUM

Tel: 32 81 61 29 35

Email: Jacquemin@cragx.fgov.be

International Triticeae EST Cooperative (ITEC)

http://wheat.pw.usda.gov/genome.
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GBX002.C11F990602#08 ITEC GBX Wheat Root Library Triticum aestivum
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Anopheles gambiae GSS T7 end of clone 25H23 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
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/dev stage="seedling, unstressed"
/clone_lib="ITEC GBX Wheat Root Library"
/note="Vector: pUCl8; 0.3-2.0 Kbp average insert size."
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Triticum aestivum"
           CDNA clone GBX002.C11, mRNA sequence. BE403103
                                                                                                       Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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AL610727.1 GI:15916912
                                                              BE403103.1 GI:9362483
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/tissue_type="Whole Plant"
/clone="trkf6d07"
/tissue_type="Whole Plant"
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                         Roux, Paris 75015, France
This close is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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500 Sunnyside Blvd., Plainview, NY 11797, USA
Tel: 516 422 4086
Fax: 516 422 4109
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/clone lib="NotreDame1"
/note="end : T7"
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Plate: tk66 row: a column: 07
High quality sequence stop: 591.
Location/Qualifiers
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/strain="PEST"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                        /organism="Anopheles
                                                                                                                                                                             Location/Qualifiers
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Woodbury Genome Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 2 : SacI
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                                                                                                          (bases 1 to 655)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehitro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehitro-chou, Teurumi-ku, Vokohama, Kanagawa 230-0045, Japan Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-041G18.F, genomic survey sequence.
AG055437
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Pan troglodytes DNA, clone: PTB-059B24.F, genomic survey sequence.
AG068743
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Direct Submission
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                                                                                    117 TTATTTTTGGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 264
73.6%; Score 36.8; DB 7; Length 591; ilarity 85.4%; Pred. No. 0.0011; Conservative 0; Mismatches 7; Indels
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
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Matches 41; Conserv
                    Local Similarity
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Louders, T. Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Birect Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1.7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

18-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Direct Submission

Bubmitted (02-AdG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (B-mail:chimpbeaggsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-135016.F, genomic survey sequence.
AG125607
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library PTB
Unpublished
    Taylor, T.D., Yada, T.,
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Fujjyama,A., Hattori,M., Toyoda,A.,
TotoKi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Tutoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:sis 1-45-503-9111, Pax:81-445-503-9170)
Glones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
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Sequencing: -21M13
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AUTHORS
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Primers AAV62497 and AAV62498 were used for the construction of the plasmid p2Z0p2J-3. The invention provides a new shuttle vector for transforming insect cells that comprises: (i) prokaryotic origin of replication; (i) insect promoter having homology to, and capible of functioning as, an immediate early baculovirus promoter; (iii)
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28-JAN-1998;
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Aa877547 DNA encod
Aa887523 DNA encod
Aa877561 DNA encod
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Aas89978 DNA encod
Aas92596 DNA encod
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(without alignments)
5419.578 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

Expression vectors for transforming insect cells from disparate lines Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bloemycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; PCR primer; ss. useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins. Hegedus DD; Pfeifer TA, Plasmid p2ZOp2J-3 constructing primer 2. Disclosure; Page 39; 121pp; English. Theilmann DA, BP (UYBR-) UNIV BRITISH COLUMBIA 97US-0049946P. 98CA-02221819. 98WO-CA000282. AAV62498 standard; DNA; 50 (first entry)

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prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/phleomycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, is useful to allow study of gene expression and direct expression of heterologous gene products, such as commercially important proteins. They are especially useful to allow expression of melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell lines from disparate species, allowing screening of lines for optimum post-translational modification of
                                                                                                                                                                                                                                                                                                                                                                         particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous
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Sequence 50 BP; 11 A; 14 C; 12 G; 13 T; 0 U; 0 Other;

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100.0%; Score 50; DB 2; I 100.0%; Pred. No. 2.4e-11;
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AAS89978 standard; cDNA; 16091 BP. AAS89978; AAS89978/c

DNA encoding novel human diagnostic protein #25782.

(first entry)

13-FEB-2002

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

Homo sapiens

WO200175067-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

HYSE-) HYSEQ INC

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73 P-PSDB; ABG25791 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 1; SEQ ID NO 25782; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food

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                      of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
supplement. (II) and its binding partners are useful in medical imaging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16091 BP; 4724 A; 3867 C; 3861 G; 3639 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                           electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No.
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23-AUG-2000; 2000US-00649167.
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Local Similarity 88.6%;
les 39; Conservative
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us-09-896-888a-10.rng

involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences Sequence 20795 BP; 4255 A; 5208 C; 5716 G; 5614 T; 0 U; 2 Other; 888888888888888

Gaps 'Match 72.0%; Score 36; DB 5; Length 20795; Local Similarity 88.6%; Pred. No. 0.00011; les 39; Conservative 0; Mismatches 5; Indels (7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50 Query Match Matches

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12363 GTTTATTGCAATCATTGCCCGCTTTCCAGTCGGGAAACCTGTCG 12406 AAA87692; 원

Human secreted protein gene 27 SEQ ID NO:37. AAA87692/c ID AAA87692 standard; cDNA; 745 BP. (first entry) 04-DEC-2000 RESULT

Human; secreted protein; immunosuppressive; immunostimulant; nootropic; antiinformatory; cardiant; vulnerary; antiulocur, antiuconvulsant; antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; cancer; immune system disorder; hyperproliferative disorder; infection; cardiovasçular disorder; hyperproliferative disorder; infection; cardiovasçular disorder; neurological disease; wound healing; ss.

Homo sapiens.

WO200043495-A2.

18-JAN-2000; 2000WO-US000903.

99US-0116330P 9-JAN-1999; (HUMA-) HUMAN GENOME SCI INC.

Ni J, Moore PA; Young PE, n SM, Ebner R, Birse CE; Ruben SM, Komatsoulis G, Rosen CA,

WPI; 2000-499225/44. P-PSDB; AAB25691 New isolated polynucleotide encoding a secreted protein useful for preventing, treating or ameliorating a medical condition.

Claim 1; Page 394; 451pp; English.

The polynucleotide sequences given in AAB25665 to AAB2708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; immunostimulant; antinflammatory; cardiant; vulnerary; antiulcer; nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective; antipacterial; antipacterial; anticonvulsant; antipacterial; antipacterial; and cytostatic. The secreted proteins and their polynucleotides can be used in gene therapy and as vaccines, chemotaxismodulators and anglogenesis- modulators. The human secreted proteins and

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Gaps

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8; Indels

71.6%; Score 35.8; DB 11; 83.3%; Pred. No. 6e-05; ive 0; Mismatches 8;

Best Local Similarity 83.3%; Matches 40; Conservative

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Query Match

Length 791;

Sequence 791 BP; 188 A; 198 C; 211 G; 182 T; 0 U; 12 Other;

site at seqdata.uspto.gov/sequence.html?DocID=20030099974

ö The invention relates to an isolated polypeptide (1) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for electecting the presence of (1) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (1) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN7981-ACN9294 represent mucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer, diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and to fight infection, AAA87657 to AAA87665 and AAB25664 represent sequences Gaps Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds. . 0 168 TTAATNGCGTTGCCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 121 71.6%; Score 35.8; DB 3; Length 745; 83.3%; Pred. No. 5.9e-05; ive 0; Mismatches 8; Indels C 20 Sequence 745 BP; 191 A; 214 C; 188 G; 142 T; 0 U; 10 Other; 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG used in the exemplification of the present invention Breast cancer related marker, seg id 7241. Disclosure; SEQ ID NO 7241; 36pp; English. Wang Y, Steinmann K; BP. 18-JUL-2002; 2002US-00198846. Query Match
Best Local Similarity 83.3%;
Marches 40; Conservative 18-JUL-2001; 2001US-0306220P (MILL-) MILLENNIUM PHARM INC ACN86091 standard; DNA; 791 02-DEC-2004 (first entry) WPI; 2003-787014/74. Lillie J, Xu Y, JS2003099974-A1. Homo sapiens ACN86091; ACN86093 g ò

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ACN83021 RESULT

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The specification describes new purified recombinant thermostable DNA polymerases having an amino acid substitution at E681. The new DNA polymerases have improved discrimination properties (and thus resulting in improved signal uniformity) and increased tolerance to high salt conditions. They also modulate the incorporation of terminators having a net positive or net negative charge during sequencing. The recombinant thermostable DNA polymerases are useful in many recombinant DNA techniques, e.g. nucleic acid amplification by polymerase chain reaction, self-sustained sequence replication, or high temperature DNA sequencing. The recombinant thermostable DNA polymerases are also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increasing the uniformity of dye-terminator incorporation in fluorescent dye DNA sequencing. The present sequence represents a sequence obtained after sequencing with a modified Tag DNA polymerase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified recombinant thermostable DNA polymerases having amino acid substitutions at E410R or E681R, useful in recombinant DNA techniques, e.g. nucleic acid amplification or high temperature DNA sequencing.
                    Thermostable DNA polymerase, signal uniformity, salt tolerance, nucleic acid amplification; polymerase chain reaction; pREFY2pref; self-sustained sequence replication; DNA sequencing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 ArriaArreceirececreaciecececrirecaeresesaacereres 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.2%; Score 35.6; DB 4; Length 327; Best Local Similarity 82.0%; Pred. No. 5.8e-05; Matches 41; Conservative 0; Mismatches 9; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 327 BP; 75 A; 82 C; 89 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Finn PJ,
                                                                                                                                                                                                                                                                                                                                                                                      (AMSH ) AMERSHAM PHARMACIA BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian cancer DNA marker #13142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Kumar S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US009126.
                                                                                                                                                                                                                                                                                                                  99US-0150167P.
99US-0154739P.
                                                                                                                                                                                                                                                                  10-AUG-2000; 2000WO-US022150
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-226620/23
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                                                                                                                                                                    WO200114568-A1
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                                                                                                                                                                                                                                                                                                               21-AUG-1999;
17-SEP-1999;
                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL39252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
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                                                                                                                                                                                                                                                                                                                                                                                        Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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71.6%; Score 35.8; DB 11; Length 869;
Best Local Similarity 83.3%; Pred. No. 6.1e-05;
Matches 40; Conservative 0; Mismatches 8; Indels 0
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                                                     544 TTAATTGCGTNGCGCTCACTGCCCGCTTTCCAGTCGGAAACCTGTCG 591
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                         TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4171; 36pp; English.
                                                                                                                                                                                                                                                                                                                                        Breast cancer related marker, seq id 4171.
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                                                                                                                                                                                             BP.
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                                                                                                                                                                                             ACN83021 standard; DNA; 869
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RESULT 7 **AAF5536**0

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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                       Homo sapiens
                                                                                                                 11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian calls. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the concerous) ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a control non-ovarian cancer. The level of expression of expression levels indicates ovarian cancer. The level of expression of a marker or a secreted protein or to a transcribed cor its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed cor its presence of the marker is a sessessed by detecting the presence of a transcribed cor its presence of the marker is a sessessed by detecting the presence of a transcribed cor its protein or protein with a marker is a sesses of by detecting the presence of a transcribed cor its protein or protein or protein with a marker is a sesses of by detecting the presence of a transcribed cor its protein or p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide which anneals with the marker or anneals with a portion of
the polynucleotide comprising the marker, under stringent conditions. The
marker is also used for monitoring the progression of ovarian cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                               Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Score 35.6; DB 5; Length 586; 82.0%; Pred. No. 6.7e-05; ive 0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 586 BP; 168 A; 131 C; 141 G; 146 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #13360.
                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 13142; 106pp; English.
                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                   2000US-0211940P.
2000US-0216820P.
2000US-0191031P
                   20,00US-0207124P
                                                                         2000US-0250661P,
2000US-0257672P,
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Best Local Similarity
                                                                                                                                                                                                             WPI; 2001-611502/70.
                                                                                                                                                                       Lillie J;
                                                                         25-JUL-2000;
21-DEC-2000;
                                     .5-JUN-2000;
                                                         07-JUL-2000;
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                                                                                                                                                                       Lee J,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). (II) repolynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the polymer of their traits to assess blodiversity and application of matains and polymerations and activity and activity and activity of the polymeration of matains and polymerations and polymerations and polymerations and polymerations are assess abidiversity and activity an
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data for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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AAS77545 standard; cDNA; 1695 BP.
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30-MAR-2001; 2001WO-US008631.
                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity 82.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                   Liu C,
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  WO200175067-A2.
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                                                  11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders olyppeptide and polymucleotide sequences have applications in disquostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations cappositions because types of data and products dependent on DNA and amino acid sequences. Abs64197-Abs94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (II) and (II) a
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Pred. No. 8.8e-05;
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2000US-00649167.
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1 Similarity 82.0%;
41; Conservative
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Best Local Similarity
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Homo sapiens
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Matches
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and contract of produce other types of date and products dependent on DNA and cannot a manification of mutations and cannot an analyse of the contracts dependent on DNA and cannot a manification of mutations and cannot an analyse of date and products dependent on DNA and cannot a manification of mutations and cannot be made and produced and cannot be made and c
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The invention relates to isolated polynucleotide (I) and polypeptide (II)
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 13351; 103pp; English.
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AAS87523 standard; cDNA; 2424 BP.
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                                        30-MAR-2001; 2001WO-US008631
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Best Local Similarity 82.0
Matches 41; Conservative
                                                                                                                                                                                                                     WPI; 2001-639362/73.
                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                      (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                               biodiversity.
                                                                                                  23-AUG-2000;
                                                                            31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1365 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2424 BP; 528 A; 721 C; 738 G; 437 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #13365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2%; Score 35.6; DB 5; 82.0%; Pred. No. 9.7e-05; iive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 23327; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS77561/c
ID AAS77561 standard; cDNA; 2710 BP
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30-MAR-2001; 2001WO-US008631.
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                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                   Tang YT;
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                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                              P-PSDB; ABG23336.
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                                                                                                                                                                                                                                                                                             biodiversity.
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Query Match
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   reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal genes. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder; contig; ds.
                                                                                                                                                                                          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1080 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1031
                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.2%; Score 35.6; DB 5; Length 2710; 82.0%; Pred. No. 9.9e-05; Live 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2710 BP; 615 A; 724 C; 690 G; 681 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 13365; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE09733 standard; DNA; 2710 BP
                                                                                     Tang YT;
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11-DEC-2001; 2001US-0339453P.
31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                      WPI; 2001-639362/73
                                                                                     Liu C,
                                                  (HYSE-) HYSEQ INC
                                                                                                                                         P-PSDB; ABG13374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VO2003054152-A2
                                                                                                                                                                                                                               biodiversity.
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                                                                                   Drmanac RT,
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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                           Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                       Zhao QA,
                                                                                                                                                                                                                                                                                                                   Zhang J, Zhao QA
ou P, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2710 BP; 615 A; 724 C; 690 G; 681 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 71.2%; Score 35.6; DB 10; Local Similarity 82.0%; Pred. No. 9.9e-05; les 41; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                            Tang YT, Asundi V, Goodrich RW, Ren F, Zhang
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P,
Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 2277; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: October 24, 2005, 18:58:10
Job time : 59.6144 secs
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-0012858.
24-APR-2002; 2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-569235/53.
                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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Page

Sequence 4171, Ap Sequence 80752, A Sequence 2086, Ap Sequence 2086, Ap Sequence 2087, Ap Sequence 13360, A Sequence 13360, A Sequence 13360, A Sequence 1337, Ap Sequence 13327, A Sequence 23327, A Sequence 23327, A Sequence 23327, A Sequence 23327, Ap Sequence 2336, Ap Sequence 2436, Ap Sequence 2436, Ap Sequence 2436, Ap Sequence 2436, Ap Sequence 347, App Sequence 347, App

Sequence 114, App Sequence 2613, A Sequence 12, Appl Sequence 1, Appl Sequence 4, Appl Sequence 44, Appli Sequence 8, Appli

Sequence 44, Appl Sequence 8, Appli

Sequence Sequence Sequence ö

Gaps

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). FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-896-888A-10
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100.0%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 50; Conservative 0; Mismatches 0; Indels
5 US-10-198-846-4171
US-09-814-351-31342
US-01-431-451-31342
US-01-632-2086
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US-10-450-763-13365
US-10-205-463-347
US-10-313-872-36
US-10-205-463-36
US-10-205-463-8
US-10-205-617-1
US-10-313-227A-44
US-10-319-227A-44
US-10-319-227A-44
US-10-319-227A-44
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Sequence 10, Application US/0989688BA

Sequence 10, Application US/098968BA

Sequence 10, US202016723A1

GENERAL INFORMATION:

TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/896,88BA

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 05/09/048,911

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
    SEQ ID NO 10
LENGTH: 50
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Sequence 25782, A
Sequence 28400, A
Sequence 37, Appl
Sequence 7241, Appl
                                                                                                                                                        ; Search time 102.023 Seconds (without alignments) 4044.488 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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4 US-10-450-763-25782
4 US-10-450-763-28400
1 US-09-985-153-37
5 US-10-198-846-7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                 9772363 seqs, 4126298632 residues
                                                                                                                                                             October 24, 2005, 20:18:24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                            IDENTITY NUC Gapox 1.0
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Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                              US-09-896-888A-10
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71.6
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Perfect score:
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Maximum DB :
                                                                                                                OM nucleic
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                                                           Length 20795;
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                                                                                                                                                                                                                                                                                            Sequence 37, Application US/0985153
Publication No. US20040181047A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFREBENCE: P2036P1
CURRENT APPLICATION WUMBER: US/09/985,153
CURRENT FILING DATE: 2001-11-01
PRIOR PILING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 745
                                                              72.0%; Score 36; DB 24;
88.6%; Pred. No. 8.2e-05;
                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (745)
; OTHER INFORMATION: n equals a, L, g, or c
US-09-985-153-37
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
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LOCATION: (93)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n = a,t,c or
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                                                                                  Best Local Similarity 88.6
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
      ; US-10-450-763-28400
                                                                                                                                                                                                                                                                                      US-09-985-153-37/c
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                                                                  Query Match
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i OTHER INFORMATION: 99% homologous to Cloning vector pBACe3.6
i OTHER INFORMATION: 1evansucrase, accession number U80929, Smith-Waterman Score=1333.
US-10-450-763-25782
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OTHER INFORMATION: 100% homologous to Cloning vector pBACe3.6
OTHER INFORMATION: levansucrase, accession number U80929, Smith-Waterman Score=110.
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                      ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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                                                                                                                                         ; Sequence 25782, Application US/10450763
; Publication Wo. US20050196754A1
; GENERAL INFORMATION:
; APPLICATION NO. US20050196754A1
; TITLE OF INVENTION:
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2001-03-30
; PRIOR PLING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; ROOFTWARE: CUSCON
; SOFTWARE: CUSCON
; SOFTWARE: CUSCON
; SOFTWARE: CUSCON
; FONTO: 16.001
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C193/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PELICATION NUMBER: 09/540,217

PRIOR PELICATION NUMBER: 09/540,167

PRIOR PELING DATE: 2000-03-31

PRIOR PILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 28400

LENGTH: 20795
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; Sequence 28400, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.6*
...nhes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: NAME/KEY: misc_feature LOCATION: (1)...(20795)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: SIMILAR
LOCATION: (961)...
                                                                                                                         US-10-450-763-25782/c
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569 TTAATTGCGTTGCGCTAACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 616
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US-10-198 846-7241

Sequence 7241, Application US/10198846

Publication No. US2030099974A1

Sequence 7241, Application US/10198846

Publication No. US2030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Wangy on Youchen

APPLICANT: Wangy Youchen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TILLE REFERENCE: MILON: THERAPY OF BREAST CANCER

FILE REFERENCE: MILON UNMER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR PLING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FASTERE FOR Windows Version 4.0

SEMOID NO 7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Mang, Youghan
APPLICANT: Wary Yongyao
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRIO49
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PAPLICATION NUMBER: 60/306,220
PRIOR PLING DATE: 2001-07-18
SOFTWARE OF SEQ ID NOS: 14084
SOFTWARE FEAKSEQ for Windows Version 4.0
SEQ ID NO 4171
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; LOCATION: 282, 300, 554, 592, 650, 707, 720, 728, 755, 767, 775, 791

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-7241
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NAME/KEY: misc_feature

LOCATION: 2, 3, 4, 6, 9, 10, 11, 531, 585, 667, 691, 696, 732, 742, 10, 10, 10, 11, 856

LOCATION: 763, 764, 780, 816, 841, 856

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-4171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.6%; Score 35.8; DB 15; Length 791; Best Local Similarity 83.3%; Pred. No. 5.4e-05; Matches 40; Conservative 0; Mismatches 8; Indels 0
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Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gaps

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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50

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GENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Exourtic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Go, Yongwei
APPLICANT: Wu, wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 80752
LENGTH: 415
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### PUDILICANT: Thompson, Pamela
### APPLICANT: Line, James
### APPLICANT: Line, James
### TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
### TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
### TITLE OF INVENTION: THERAPY OF O'OVARIAN CANCER
### TITLE OF INVENTION: THERAPY OF O'OVARIAN CANCER
### TITLE OF INVENTION: THERAPY OF O'OVARIAN CANCER
### TILM APPLICATION NUMBER: US 60/191,031
### PRIOR FILING DATE: 2000-03-21
### PRIOR FILING DATE: 2000-03-21
### PRIOR FILING DATE: 2000-05-25
### PRIOR PELING DATE: 2000-05-25
### PRIOR FILING DATE: 2000-06-15
### PRIOR FILING DATE: 2000-07-07
### PRIOR FILING DATE: 2000-07-05
### PRIOR FILING DATE: 2000-07-05
### PRIOR FILING DATE: 2000-07-07
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Best Local Similarity 82.0%; Pred. No. 5.9e-05;
Matches 41; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_80346C.1
US-10-437-963-80752
; Sequence 80752, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 13142
LENGTH: 586
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PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(865)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-027-632-2086/c
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ORGANISM: Human
                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                  SEQ ID NO 2087
LENGTH: 865
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                                                                                                                                                                                                                       Sequence 2086, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICATT WANG, David G

TITLE OF INVENTION: 1dentification and Mapping of Single Nucleotide

TITLE OF INVENTION: 1dentification and Mapping of Single Nucleotide

TITLE OF INVENTION: 1dentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

TITLE OF INVENTION: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PELICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-00-24

PRIOR PELICATION NUMBER: US 60/166,363

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PELICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR SEC ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: PARKEN ARE
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                                                                                                                       516 ATTTAATTGCGTTGGCCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
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              Score 35.6; DB 10; Length 586;
Pred. No. 6.3e-05;
0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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US-10-027-632-2086
          ch 71.2%;
l Similarity 82.0%;
41; Conservative
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Best Local Similarity 82.0%;
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            Query Match
Best Local Similarity
Matches 41; Conservat
                                                                                                                                                                                                                   -10-027-632-2086/c
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US-10-027-632-2087/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome
FITTLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
FRIOR PILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-13,483
FRIOR PILING DATE: 2000-02-29
FRIOR APPLICATION NUMBER: US 60/183,483
FRIOR APPLICATION NUMBER: US 60/165,363
FRIOR APPLICATION NUMBER: US 60/165,363
FRIOR APPLICATION NUMBER: US 60/166,363
FRIOR APPLICATION NUMBER: US 60/166,363
FRIOR APPLICATION NUMBER: US 60/166,363
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR PILING DATE: 1999-09-28
FRIOR PILING DATE: 1999-09-09-28
FRIOR FILING DATE: 1999-09-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-08
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                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR TILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(865)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2087
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OTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 1695
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PLING DATE: 2000-03-30

PRIOR PLING DATE: 2000-03-31

PRIOR PLING DATE: 2000-03-31

PRIOR PLING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSTOM

LENGTH: 1637
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Publication No. US20050196754A1
GENERAL INFORMATION:
Sequence 2087, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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LOCATION: (1)...(865)

OTHER INFORMATION: n = A,T,C or G

US-10-027-632-2087
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ORGANISM: Homo sapiens
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LOCATION: (241)..(849)
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ORGANISM: Human
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FEATURE:
NAME/KEY: SIMILAR
LOCATION: (85)..(2142)
OTHER INFORMATION: 97% homologous to Homo sapiens putative p150, accession number
OTHER INFORMATION: U93563, Smith-Waterman Score=3485.
OTHER INFORMATION: 100% homologous to Homo sapiens endoglycan, accession number OTHER INFORMATION: AF219137, Smith-Waterman Score=1070.
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71.2%; Score 35.6; DB 24; Length 1695;
Best Local Similarity 82.0%; Pred. No. 7.6e-05;
Matches 41; Conservative 0; Mismatches 9; Indels 0;
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                                                                                                                                                                                                                                   Length 1637;
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Sequence 13349, Application US/10450763

Sequence 13349, Application US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REPERENCE: 790C1P3/US

CURRENT APLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR PILING DATE: 2000-03-10

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CURLED NOS: 60736
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                       Query Match 71.2%; Score 35.6; DB 24; Best Local Similarity 82.0%; Pred. No. 7.6e-05; Matches 41; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4942, Application US/10450763; Publication No. US20050196754A1; GENERAL INFORMATION:
                                                                             | NAME/KEY: misc_feature
| LOCATION: (1)...(1637)
| OTHER INFORMATION: n = a,t,c or g
| US-10-450-763-13360
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LOCATION: (1).T.(1695)
CTHER INFORMATION: n = a,t,c or g
US-10-450-763-13349
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PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 4942
LENGTH: 1942
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1514)... (1942)
OTHER INPORMATION: 100% homologous to Cloning vector psacBII SacB, accession
CTHER INPORMATION: number U09128, Smith-Waterman Score=768.
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Search completed: October 25, 2005, 06:13:42 Job time : 106.689 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-322-730A-114
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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COMPUTER: USA
ZIP: 92121-4362
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM compatible
COMPUTER: ADVILOATION DATA:
PRING APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/221,804
FILING DATE: April 1, 1994
ATTORNY/AGENT INFORMATION:
NAME: CHAISEINE A. GATLERMACHER
REGISTRATION NUMBER: 40,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08778217; Patent No. 5935833; GENERAL INFORMATION:
TITLE OF INVENTION: Highly-Purified Recombinant TITLE OF INVENTION: Reverse Transcriptase; NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.2; DB 2;
Pred. No. 9.6e-06;
0; Mismatches 8;
US-09-702-705-639
US-09-736-447-639
US-09-614-124-639
US-09-614-124-639
US-09-589-114-639
US-09-589-114-639
US-09-334-818A-10
US-09-334-818A-16
US-09-334-818A-16
US-09-334-818A-16
US-09-334-818A-17
US-09-334-818A-19
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US-09-334-818A-15
US-09-334-818A-15
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REFERENCE/DOCKET NUMBER: MOL2A-A01F01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LELEFHONE: (619) 410-8926
TELEFAX: (619) 410-8928
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 40; Conservative (
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STATE: California
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US-08-778-217-1
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US-09-397-955C-1
                                                                                                                                                                                                                              TYPE: DNA
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APPLICANT: RIGGS, Michael G.
APPLICANT: SCRENSEN, Matthew
APPLICANT: SORBNESN, Matthew
TITLE OF INVENTION: RECOMBINANT DNA ENCODING REVERSE TRANSCRIPTASE DERIVED FROM
TITLE OF INVENTION: MOLONEY MURINE LEUKEMIA VIRUS
FILE REFERENCE: GPOS9-05.CP1
CURRENT APPLICATION NUMBER: US/09/397,955C
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 08/821,948
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/221,804
FILING DATE: May 18, 1995
APPLICATION NUMBER: 08/221,804
FILING DATE: April 1, 1994
ATTORNEY AGENT INCRMATION:
NAME: Christine A. Gritzmacher
REGISTRATION NUMBER: 40,627
REFERENCE/DOCKET NUMBER: 40,627
REFERENCE/DOCKET NUMBER: 6(19) 410-8926
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 410-8928
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.4%; Score 35.2; DB 2; Length 114; llarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels (
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||||| TAATTGGTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 16
                                                                                                                US-08-81-948-1/c
| Sequence 1, Application US/08821948|
| Patent No. 599195|
| GENERAL INFORMATION:
| APPLICANT: Kacian et al. |
| TITLE OF INVENTION: Highly-Purified Recombinant |
| TITLE OF INVENTION: Reverse Transcriptase |
| NUMBER OF SEQUENCES: 13 |
| CORRESPONDENCE ADDRESS: CARRESTEE: Gen-Probe Incorporated |
| STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92121-34362
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft MS-DOS (Version 6.0)
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,948
FILING DATE: March 22, 1997
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Patent No. 6593120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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CITY: San Diego
STATE: California
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Best Local Similarity
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APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.4%; Score 35.2; DB 4; Length 114; Best Local Similarity 83.3%; Pred. No. 9.6e-06; Matches 40; Conservative 0; Mismatches 8; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HIGHLY-PURIFIED RECOMBINANT REVERSE TITLE OF INVENTION: TRANSCRIPTASE NUMBER OF SEQUENCES: 18 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04092
FILING DATE:
CLASSIFICIAL:
INFORMATION PAPEL
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB 5;
Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TTAAGCTTATAGCGATGACTGCCCGCTT
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION WINBER: 08/443,781
PRIOR FILING DATE: 1995-05-18
PRIOR APPLICATION NUMBER: 08/221,804
PRIOR PLING DATE: 1994-04-01
SUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-04092-1/c; Sequence 1, Application PC/TUS9504092; GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-276-852-41/c
; Sequence 41, Application US/08276852
Patent No. 5652138
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-04092-1
                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 40; Conservative
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PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
PRIOR APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION NUMBER: US 07/826,623
FILING DATE: 10-APR-1992
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
                                                                                                                                                                                                                                                                                                                                                                                             SCRF 238.2
                                                                                                                                                                                                                                                                                     PCT/US 92/03091
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
                                                            08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                 FILING DATE: 08 CLASSIFICATION:
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                                         SOFTWARE
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SSEB: Patent Counsel
T: 10666 No. 5652138th Torrey Pines Road, Suite 220, Is a Jolla
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 114.17, Application US/08133011
Patent No. 5658727
GENERAL INFORMATION:
APPLICANT: Kang, Angray
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                       ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Patent Counsel
STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
                                                                                                                                                                                              COMPUTER FALSABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elba PC Compatible
OPERATING SYSTEM: PC-0DS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
RIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTOKNED FASSEL TO THOMAS

REGISTRATION NUMBER: 34,163

REPERENCE/DOCKET NUMBER: SCR1452P
TELECHMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CA
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MOLECULE TYPE: DN
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                                                                                                                                                                                   92037
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                                                                                               STREET: NCITY: La STATE: CACOUNTRY:
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Gaps
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Sequence 114, Application US/08322730A

Patent No. 575981.

Sequence 11712 OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING TITLE OF INVENTION: PHAGEMIDS

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: The SCTIPUS Research Institute, Office of ADDRESSEE: Patent Counsel

STREET: 10550 No. 5759817th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8

CITY: La Johla

STREET: CA.
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Query Match 70.4%; Score 35.2; DB 1; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                       65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 18
                                                                                                                        3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,730A
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 83.3%;
Matches 40; Conservative (
                                                                                                        Query Match
Best Local Similarity 83.37
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                  RESULT 9
US-08-899-575-41/c
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                                                , ANTI-SENSE:
US-08-387-874-87
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Fatent No. 5770356

Fatent No. 5770356

Fatent No. 11364.

APPLICANT: Light, Paul L., II

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: PHAGBMIDS COEXPRESSING A SURFACE

TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN

NUMBER OF SEQUENCES. 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFIGURATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,874
FILING DATE: 22-FEB-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,369
FILING DATE: 04-SEP-1992
ATORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: TSRI 303.1
TELECHOME: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.2; DB 1;
Pred. No. 1.1e-05;
0; Mismatches 8;
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR0707P
TELECHONE: 619-784-2937
TELEPHONE: 619-784-2939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-
                                                                                                                                  TELEFAX: 619-784-9399
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                La Jolla
CA
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US-08-322-730A-114
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Burton, Dennis R
APPLICANT: Burton, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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Score 35.2; DB 1; Length 201; Pred. No. 1.1e-05; 0; Mismatches 8; Indels C
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                                                                                               3 TTAAGCTTATAGCGATGACTGCCCCCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                       65 rraarrecerrecercacrecececrirecagreggaaaccrere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FTI.ING DATE: 24-UUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                    Sequence 41, Application US/08899575; Patent No. 5770440; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
    70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Burton, Carlos F
APPLICANT: Burton, Seriard S
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN INMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: LA JOILA
STREET: CA
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70.4%; Score 35.2; DB 1; Length 201;
Best Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 40; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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                                               65 traatrgcgtrgcgcrcacrgccgcrrrccagrcggaaacc
TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPUTER: IBM PC compatible
OERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                             Sequence 41, Application US/08899575
Patent No. 5804440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Sequence 114, Application US/08383619; Patent No. 5955341

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Patent No. 6235469
GENERAL INFORMATION:
APPLICANT: Kang, Angray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
                                                                 HETERODIMERIC RECEPTOR LIBRARIES USING PHAGEMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                            ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,619
FILING DATE:
                                                                                                                                                               ADDRESSEE: DOUGLAS A. BINGHAM
STREET: 11300 Sorrento Valley Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB 2;
Pred. No. 1.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR0371P
TELECOMMUNICATION INFORMATION:
TELERHONE: 619-546-1555
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: APPLICATION NUMBER: US/07/683,602
APPLICANT: Kang, Angray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard
ITILE OF INVENTION: HETERODIN
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSE: DOUGLAS A. BINGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 83.3%;
Matches 40; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States
                                                                                                                                                                                                                  CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 10666 PCITY: La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-907-739-114/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-383-619-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: C. COUNTRY: ZIP: 920:
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PHAGEMIDS COEXPRESSING A SURFACE RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 Traatrecerrecercecececreces 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.4%; Score 35.2; DB 3; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8;
                      APPLICATION NUMBER: 08/133,011
FILING DATE: 1994-09-29
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAM-1992
APPLICATION NUMBER: PCT/US 92/03091
PILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,369
FILING DATE: 04-SEP-1992
INFORMATION FOR SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
PCT-US93-08364-87/c
; Sequence 87, Application PC/TUS9308364
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PHAC
TITLE OF INVENTION: RECE
NUMBER OF SEQUENCES: 97
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 40; Conservative
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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Patent No. 6468738

GENERAL INFORMATION:
APPLICANT: Kang, Angray
Barbas, Carlos
Lerner, Archard A.

TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
PHAGEMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGAAACCTGTCG 18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; DB 3;
Pred. No. 1.1e-05;
0; Mismatches 8;
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RAPPLICATION NUMBER: US/09/729,597
FILING DATE: 04-Dec-2000
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-3AN-1992
PRIOR APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-3AN-1992
ATTONNEY,AGENT 10-APR-1992
ATTONNEY,AGENT 10-APR-1992
ATTONNEY,AGENT 1NFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 70.4%;
1 Similarity 83.3%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-729-597-114/c
                                                                                                                                                                            FILING DATE:
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RESOURT 15
PCT-US95-08743-41/C
Sequence 41, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: TO HUMAN INMUNOBERICIENCY VIRUS
INTELE OF INVENTION: TO HUMAN INMUNOBERICIENCY VIRUS
TITLE OF INVENTION: TO HUMAN INMUNOBERICIENCY VIRUS
COMPUTER: READABLE FORM:
MEDIUM TYPE: PLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
PTLING DATE: 11-JUU-1995
PRIOR APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 18-JUL-1994
INFORMATION POR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-08743-41
RESULT 15
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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50

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Query Match 70.4%; Score 35.2; DB 5; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels (

Search completed: October 24, 2005, 21:57:51 Job time : 19.0038 secs

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